

CC produce 2 different mRNAs, one encoding a long form (bcl-XL), the
CC other a short form (bcl-XS), lacking a stretch of 63 amino acids,
CC by differential splicing of the 2nd coding exon to a more proximal
CC 5'-splice donor within the 1st coding exon. Bcl-XS acts as a
CC dominant negative regulator to bcl-XL activity, so it is preferable
CC to use the bcl-XL cDNA for expression. The gene may be modified to
CC facilitate interaction with costimulatory Bax protein and inhibit
CC interaction with antagonistic Bad protein, by modification of the
CC Bcl-2 homology domains BH1 and/or BH2. The bcl-XL gene may be
CC introduced into T-cells in vivo or ex vivo via gene transfer using
CC a vector for HIV infection gene therapy, to augment intracellular
CC bcl-XL protein levels and protect from cell death. A corresponding
CC antisense oligonucleotide or expression vector may be used in gene
CC therapy of e.g. autoimmune disease, graft rejection or graft-
CC versus-host disease, to induce cell death (e.g. apoptosis) and
CC down-regulate the immune response in a T-lymphocyte population.
CC Sequence 926 BP; 220 A; 249 C; 264 G; 193 T;
SQ

Query Match 22.5%; Score 131; DB 1; Length 926;
Best Local Similarity 56.3%; Pred. No. 8.7e-24;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
QY 98 ccggggagggccagcagctgacccgctgcacaaagccatgcccgcgtggagatgagt 157
DB 364 cccggagggtgatccccatggcagcagcagtaaaagcaagcgtgaggagcagcgcagcag 423
QY 158 tgaagaccgcttcggcgaccctctctgctgctgagggcgtcagctgacatgaccccg 217
DB 424 ttgaactgcggtacccggcgccatttcagtgacctgacatccacgtccacatcccccag 483
QY 218 gctcagccagcaacgctccacccaggtctccgacgaacttttcaaggggggccccaact 277
DB 484 gcacagcatatcagagcctttgaacaggtagtgatgaactcttccgggatggcgtaaaact 543
QY 278 ggggcccgtttagctctcttcttcttggggcgtcactgtgtgctgagagtgtaaca 337
DB 544 ggggtgcgatttgcccttttcttcttccggcgccacttgcgttggaagcgtagaca 603
QY 338 agagatgaacacactgtggacaagtgcagagtgatggtggtcctacctgagagcgc 397
DB 604 agagatgcaggtattgtgtgagtcggatcgagcttgatggatgccacatctgactgac 663
QY 398 ggcctgctcagctggatccacagcagtgagggtggggcgtggttcacagctctatacggg 457
DB 664 acctagagccttgatccaggagacgcgcgtgggatacttttctggaactctatggga 723
QY 458 acggggccctggagagcgcgcgtctgctggggagggagaaactgggcatcagtgaggacag 517
DB 724 acaatgcagacccgagagccgaaaggccaggaacgcttcaacgcgtggttctctgacgg 783
QY 518 tgcagcggggccg 532
DB 784 gcactgactggtggcg 798

RESULT 15

X33182
ID X33182 standard; DNA; 7372 BP.
AC X33182;
DT 25-JUN-1999 (first entry)
DE Base sequence of the plasmid pRc-Bcl-XL-bcr.
KW Cowpox virus; bcr; viral vector; expression; apoptosis; resistance;
KW crmA; bcl-2; bcl-XL; FLIP; survivin; IAP; adenovirus; cancer;
KW autoimmune disease; graft rejection reaction; inflammation;
KW inflammatory disease; ss.
OS Synthetic.
OS Homo sapiens.
PN W0913073-A2.
PD 18-MAR-1999.
PF 07-SEP-1998; J04010.
PR 08-SEP-1997; JP-259235.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.

PI Hamada H;
DR WPI: 99-243728/20.
PT New apoptosis-resistant virus-sensitive cell
PS Example 2; Page 41-45; 51pp; English
CC The present invention describes an apoptosis-resistant virus-sensitive
CC cell line into which an apoptosis resistance gene has been introduced.
CC The recombinant viruses generated are capable of expressing apoptosis-
CC associated genes. These can then be used in a variety of diseases for
CC which the induction of apoptosis by gene transfer, or where the
CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
CC are useful as vectors for gene therapy which can be applied to cancer
CC therapy for destroying cancer cells selectively, the treatment of
CC autoimmune diseases and graft rejection reaction, and apoptosis induction
CC therapy for inflammatory cells in adenovirus vector capable of
CC encountered the problem where if an adenovirus vector capable of
CC expressing an apoptosis-associated gene is introduced into animal cells,
CC the cells producing the virus will be destroyed because the period of
CC time required to induce cell death by apoptosis is shorter than that
CC required to replicate and produce the virus, resulting in failure to
CC obtain a recombinant virus having the integrated apoptosis-associated
CC gene. In this invention an apoptosis-resistant 293 cell line (having an
CC apoptosis resistant gene introduced) is established and overcomes the
CC problem. The present sequence represents the base sequence of the
CC plasmid pRc-Bcl-XL-bcr, which contains the human Bcl-XL gene, and
CC is used in an example from the present invention.
CC Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T;
SQ

Query Match 22.5%; Score 131; DB 1; Length 7372;

Best Local Similarity 56.3%; Pred. No. 1.3e-23;

Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 ccggggagggccagcagctgacccgctgcacaaagccatgcccgcgtggagatgagt 157
DB 2302 cccggagggtgatccccatggcagcagtaaaagcaagcgtgaggagcagcgcagcag 2361
QY 158 tcagagaccgcttcggcgaccctctctgctgctgagggcgtcagctgcatgagaccccg 217
DB 2362 ttgaactgcggtacccggcgccatttcagtgacctgacatccacgtccacatcccccag 2421
QY 218 gctcagccagcaacgcttcacccaggtctccgacgaacttttcaaggggggccccaact 277
DB 2422 gcacagcatatcagagcctttgaacaggtagtgatgaactcttccgggatgggtaaaact 2481
QY 278 ggggcccgtttagctctcttcttcttggggcgtcactgtgtgctgagagtgtaaca 337
DB 2482 ggggtgcgatttgcccttttcttcttccggcgccacttgcgttggaagcgttagaca 2541
QY 338 agagatgaacacactgtggacaagtgcagagtgatggtggtggtcctacctggagacgc 397
DB 2542 agagatgcaggtattgtgtgagtcggatcgacgttggatggccactttacctgaatgacc 2601
QY 398 ggcctgctcagctggatccacagcagtgagggtggggcgtgggagttcacagctctatacggg 457
DB 2602 acctagagccttgatccaggagacgcgcgtgggatacttttctggaactctatggga 2661
QY 458 acggggccctggagagcgcgcgtctgctggggagggagaaactgggcatcagtgaggacag 517
DB 2662 acaatgcagacccgagagccgaaaggccaggaacgcttcaacgcgtggttctctgacgg 2721
QY 518 tgcagcggggccg 532
DB 2722 gcactgactggtggcg 2736

Search completed: July 4, 2000, 01:26:24
Job time: 14671 sec

Qy 421 agtgggggctgg 432
| | | | | | | | | |
Db 421 AGTGGGGGCTGG 432

RESULT 12
V59630
ID V59630 standard; DNA; 1864 BP.
AC V59630;
DE 19-JAN-1999 (first entry)
KW Human secreted protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumor; neurodegenerative disorder; leukemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN W09839448-A2.
PD 11-SEP-1998.
PF 06-MAR-1998; U04493.
PR 02-OCT-1997; US-061060.
PR 07-MAR-1997; US-038621.
PR 07-MAR-1997; US-040161.
PR 07-MAR-1997; US-040162.
PR 07-MAR-1997; US-040163.
PR 07-MAR-1997; US-040333.
PR 07-MAR-1997; US-040334.
PR 07-MAR-1997; US-040336.
PR 07-MAR-1997; US-040626.
PR 11-APR-1997; US-043311.
PR 11-APR-1997; US-043312.
PR 11-APR-1997; US-043313.
PR 11-APR-1997; US-043314.
PR 11-APR-1997; US-043568.
PR 11-APR-1997; US-043569.
PR 11-APR-1997; US-043576.
PR 11-APR-1997; US-043578.
PR 11-APR-1997; US-043580.
PR 11-APR-1997; US-043669.
PR 11-APR-1997; US-043670.
PR 11-APR-1997; US-043671.
PR 11-APR-1997; US-043672.
PR 11-APR-1997; US-043674.
PR 23-MAY-1997; US-047492.
PR 23-MAY-1997; US-047500.
PR 23-MAY-1997; US-047501.
PR 23-MAY-1997; US-047502.
PR 23-MAY-1997; US-047503.
PR 23-MAY-1997; US-047581.
PR 23-MAY-1997; US-047582.
PR 23-MAY-1997; US-047583.
PR 23-MAY-1997; US-047584.
PR 23-MAY-1997; US-047585.
PR 23-MAY-1997; US-047586.
PR 23-MAY-1997; US-047587.
PR 23-MAY-1997; US-047588.
PR 23-MAY-1997; US-047589.
PR 23-MAY-1997; US-047590.
PR 23-MAY-1997; US-047592.
PR 23-MAY-1997; US-047593.
PR 23-MAY-1997; US-047594.
PR 23-MAY-1997; US-047595.
PR 23-MAY-1997; US-047596.
PR 23-MAY-1997; US-047597.
PR 23-MAY-1997; US-047598.
PR 23-MAY-1997; US-047599.
PR 23-MAY-1997; US-047600.
PR 23-MAY-1997; US-047601.
PR 23-MAY-1997; US-047612.
PR 23-MAY-1997; US-047613.

PR 23-MAY-1997; US-047614.
PR 23-MAY-1997; US-047615.
PR 23-MAY-1997; US-047617.
PR 23-MAY-1997; US-047618.
PR 23-MAY-1997; US-047632.
PR 23-MAY-1997; US-047633.
PR 06-JUN-1997; US-048964.
PR 06-JUN-1997; US-048974.
PR 13-JUN-1997; US-049610.
PR 08-JUL-1997; US-051926.
PR 16-JUL-1997; US-052874.
PR 18-AUG-1997; US-055724.
PR 22-AUG-1997; US-056630.
PR 22-AUG-1997; US-056631.
PR 22-AUG-1997; US-056632.
PR 22-AUG-1997; US-056636.
PR 22-AUG-1997; US-056637.
PR 22-AUG-1997; US-056662.
PR 22-AUG-1997; US-056664.
PR 22-AUG-1997; US-056845.
PR 22-AUG-1997; US-056862.
PR 22-AUG-1997; US-056864.
PR 22-AUG-1997; US-056872.
PR 22-AUG-1997; US-056874.
PR 22-AUG-1997; US-056875.
PR 22-AUG-1997; US-056876.
PR 22-AUG-1997; US-056877.
PR 22-AUG-1997; US-056878.
PR 22-AUG-1997; US-056879.
PR 22-AUG-1997; US-056880.
PR 22-AUG-1997; US-056881.
PR 22-AUG-1997; US-056882.
PR 22-AUG-1997; US-056884.
PR 22-AUG-1997; US-056886.
PR 22-AUG-1997; US-056887.
PR 22-AUG-1997; US-056888.
PR 22-AUG-1997; US-056889.
PR 22-AUG-1997; US-056892.
PR 22-AUG-1997; US-056893.
PR 22-AUG-1997; US-056894.
PR 22-AUG-1997; US-056903.
PR 22-AUG-1997; US-056908.
PR 22-AUG-1997; US-056909.
PR 22-AUG-1997; US-056910.
PR 22-AUG-1997; US-056911.
PR 05-SEP-1997; US-057650.
PR 05-SEP-1997; US-057659.
PR 05-SEP-1997; US-057761.
PR 12-SEP-1997; US-058785.
PR (HUMA-) HUMAN GENOME SCI INC.
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
DR WPI; 98-506364/43.
DR P-PSDB; W74648.
DR New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS Claim 1: Page 353-354; 721pp; English.
CC This sequence represents a nucleic acid molecule designated Gene 120 from
CC the human cDNA clone HBGZ64 (deposited as clone ATCC 97902 and ATCC
CC 209048) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. V59502) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on


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Db 361 CAAGTGCAGGATTGGATGGTACCTACTGGAGACAGCTGGCTGACTGGATCCACAGC 420
QY 421 agtgggggctggcgaggttcacagctctatcacgggacggggccctggagagggcgcg 480
Db 421 AGTGGGGCTGGCGGAGTTCAACAGCTCTATACGGGACGGGGCCCTGGAGGAGGACGG 480
QY 481 cgtctcgagggaggaactgggcatcagtgagagacagtgctgacggggcgctggcactg 540
Db 481 CGTTCGGGGAGGGGAACCTGGGATCAGTGAGGACAGTGTGACGGGGGCTGTGGCACTG 540
QY 541 ggggcccctgtaactgtagggccttttttctagcaag 579
Db 541 GGGCCCCGTGTAAGTGTAGGGGGCTTTTTCGTAGCAAG 579

RESULT 7
X15945
ID X15945 standard; cDNA; 579 BP.
AC X15945;
DT 20-MAY-1999 (first entry)
DE cDNA encoding the rat bcl-2 protein.
KW Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Rbcl-2; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite; ss.
OS Rattus sp.
PN US883229-A.
PD 16-MAR-1999.
PF 23-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PI (COCE-) COGENSYS INC.
PI Guastella J;
DR WPI; 99-214150/18.
DR P-PSDB; W97391.
PT Novel bcl-2 homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
PS Disclosure: Columns 13-16: 26pp; English.
CC The present sequence encodes rat bcl-2 protein (Rbcl-2). The
CC specification also describes human bcl-2 protein (Hbcl-2). Rbcl-2 and
CC Hbcl-2 are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-2 and Hbcl-2 may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites.
CC Sequence 579 BP; 111 A; 157 C; 198 G; 113 T;

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Query Match 89.7%; Score 523; DB 1; Length 579;
Best Local Similarity 94.0%; Pred. No. 2.1e-120;
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atggcgacccagctggcgccacacacagcgctctggggcagactttgtaggttat 60
Db 1 ATGGCGACCCCGCTCAACCCCGACACACGGGCTAGTGGCTGACTTGTAGGCTAT 60

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QY 61 aagctgagggcagaaggggttatgtctgtgagctggcccgggagggcccgagcagctgac 120
Db 61 AAGCTGAGACAGAAGGGTTATGTCTGTGAGCTGCCCTGGGGAAGGCCAGCAGCCGAC 120
QY 121 cggctgcaccaagccatcgggcagctggagatgagttcgagaccgcttcccgcgacc 180
Db 121 CCGCTGCAACCAAGCCATCGGGCAGCTGGAGACGAGTTTGGAGACCCGCTTCCGGGCAACC 180
QY 181 ttctctgactctggcgctcagctgcatgtgaccccgagctcagcccgacagcagcttacc 240
Db 181 TTCTCTGACCTGGCGCTCAGCTACGTCAGCCCGAGGCTCAGCCCGACAGCGCTTCACC 240
QY 241 caggtctccgacgaacttttcaaggggggcccaactgggcccgtttagccttttt 300
Db 241 CAGGTTTCCGACGAACCTTTTCCAGGGGGGCCCAACTGGGCGCTTGTGTGGCATTCCTT 300
QY 301 ctctttgggggctgcaactgtgtgctgagagtgatcaacaaggagatggaacccactgggga 360
Db 301 GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGGAGCCATTGGTGGGA 360
QY 361 caagtgcaggagtgatgtgtgctacctgagacgcgctggtcgactggtatccacagc 420
Db 361 CAAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACACCTTGGCTGACTGGATCCACAGC 420
QY 421 agtgggggctggcgagtgatcacagctctatcacggggacggggccctggagagggcgcg 480
Db 421 AGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGGACGGGCCCTGGAGAGGACGCGG 480
QY 481 cgtctcgagggggaactgggcatcagtgagagcagtgctgacggggcgctggcagctg 540
Db 481 CGTCTGCGGGGAGGGAACCTGGGCACTCAGTGAGGACAGTGTGACGGGGGCTGTGGCACTG 540
QY 541 ggggcccctgtaactgtaggggcccctttttctagcaag 579
Db 541 GGGGCCCTGTGTAAGTGTAGGGGGCTTTTTCGTAGCAAG 579

RESULT 8
X25133
ID X25133 standard; DNA; 581 BP.
AC X25133;
DT 05-JUL-1999 (first entry)
DE Mouse bcl-2 gene.
KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW animal model; ss.
OS Mus sp.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1997; AU-009228.
PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR P-PSDB; Y05531.
PT An animal model exhibiting reduced levels of a Bcl-2 protein and/or
PT protein associated with Bcl-2
PS Claim 3; Page 34; 52pp; English.
CC The present sequence is the mouse bcl-2 gene encoding Bcl-2 protein
CC (see Y05531), a pro-survival member of the Bcl-2 family which is
CC widely expressed and which is essential for spermatogenesis. The
CC invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male
CC animals. Methods are provided for the treatment of infertility, or
CC for reducing fertility, by modulating spermatogenesis. An animal
CC model carries a mutation is at least one allele of the human or
CC murine bcl-2 gene or in a gene associated with bcl-2. Such animals
CC have disorganised seminiferous tubules and are substantially
CC infertile, but possess no other major abnormalities as determined
CC by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of
CC inducing, enhancing or otherwise facilitating spermatogenesis in
CC animals, or which can induce infertility.

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OS Homo sapiens.
PN US5883229-A.
PD 16-MAR-1999.
PF 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J.
DR WPI; 99-214150/18.
DR P-PSDB; W97392.
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
PS Disclosure; Columns 15-16; 26pp; English.
CC The present sequence encodes human bcl-y protein (Hbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites.
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T;

Query Match 97.4%; Score 567.8; DB 1; Length 579;
Best Local Similarity 98.8%; Pred. No. 1.9e-131;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 atggcgacccagctcgcccccagacacagcgctctgtggcagactttaggttat 60
DB 1 ATGGCGACCCAGCTCGCCCCAGACACAGCGCTCTGTGGAGAGACTTGTAGGTAT 60
QY 61 aagctgagcgagaaggttatgtctgtgagctggcccccggggggcccgagcagctgac 120
DB 61 AAGCTGAGCGACAGAGGTTATGTCTGTGGAGCTGSCCCCGGGAGGGCCAGCAGCTGAC 120
QY 121 ccgctgacccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
DB 121 CCACCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTTCGAGACCCGCTTCGGCGCAC 180
QY 181 ttctctgactgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
DB 181 TTCTCTGATCTCGCGCTCAGCTGATGATGACCCAGCTCAGCCACACACAGCTTAC 240
QY 241 caggtctccgacgaacttttcaaggggggggggggggggggggggggggggggggggg 300
DB 241 CAGGCTCTCGATGAACCTTTTCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 300
QY 301 ctctttgggggctgactgtgtgtgagagtgatgacaaaggagatggaacactggtggga 360
DB 301 GTCTTTGGGGCTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 caagtgcaggagtgatggtgacctacactgagacgagcagcagcagcagcagcagcagc 420
DB 361 CAAGTGCAGGAGTGTGATGGTGGCTTACTTGAGACCGCGCTGGCTGACTGATCCACAG 420
QY 421 agtgggggctggcgaggttcaacagctctatacgggggggggggggggggggggggggg 480
DB 421 AGTGGGGCTGGCGAGTTCACAGCTCTATACGGGGGAGCGGGGGGGGGGGGGGGGGGG 480
QY 481 cgtctgcggggaaggaactgggcatcagtgaggacagtgctgacgggggggggggggggg 540
|||||

Db 481 CGTCTCGGGAGGGGAACCTGGGCATCAGTCAGACAGTCTGACGGGGGCCGTGGCACTG 540
QY 541 gggccctgtaactgtagggccttttttttctagcaag 579
Db 541 GGGGCCCTGTAACCTGTAGGGCCCTTTTGTCTAGCAAG 579
RESULT 6
V28333
ID V28333 standard; cDNA; 579 BP.
AC V28333;
DE 02-OCT-1998 (first entry)
DT Rat bcl-y gene.
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 1..579
FT /tag= a
FT /product= bcl-y
FT /note= "No stop codon given"

PN US5789201-A.
PD 04-AUG-1998.
PF 11-FEB-1997; 798897.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PA (COCE-) COCENSYS INC.
PI Guastella J.
DR WPI; 98-446079/38.
DR P-PSDB; W61391.
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
PS Claim 2; Column 13/14; 27pp; English.
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family
CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontrolled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired.
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T;

Query Match 89.7%; Score 523; DB 1; Length 579;
Best Local Similarity 94.0%; Pred. No. 2.1e-120;
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atggcgacccagcctcgcccccagacacacagcgctctgtggcagactttaggttat 60
DB 1 ATGGCGACCCAGCCTCAACCCAGACACACAGCGGCTCTAGTGGCTGACTTGTAGCTAT 60
QY 61 aagctgagcgagaaggttatgtctgtgagctggcccccgggggggggggggggggggggg 120
DB 61 AAGCTGAGACAGAGGTTATGTCTGTGGAGCTGGCCCTTGGGGAAGCCAGCAGCGAC 120
QY 121 ccgctgacccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
DB 121 CCGCTGCACCAAGCCATGCGGCGAGCTGGAGACAGTTTGGAGACCCGCTTCGGCGCAC 180
QY 181 ttctctgactgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
DB 181 TTCTCTGACTGGCGCTCAGCTACACGTACCCAGCTCAGCCAGCCAGCAGCTTAC 240
QY 241 caggtctccgacgaacttttcaaggggggggggggggggggggggggggggggggggg 300
DB 241 CAGGTTCCAGCAACCTTTTCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 300
QY 301 ctctttgggggctgactgtgtgtgagagtgatgacaaaggagatggaacactggtggga 360
DB 301 GTCTTTGGGGCTGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 caagtgcaggagtgatggtgacctacactgagacgagcagcagcagcagcagcagcagc 420
|||||

CC inducing, enhancing or otherwise facilitating spermatogenesis in
 CC animals, or which can induce infertility.
 SQ Sequence 581 BP; 104 A; 155 C; 210 G; 112 T;

Query Match 98.3%; Score 573; DB 1; Length 581;
 Best Local Similarity 99.1%; Pred. No. 1e-132;
 Matches 576; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 atggcagccagcctggcccccagacacacagcggctctgtgagcagactttgtaggttat 60
 Db 1 ATGGGACCCAGCCTGGGCCCCAGACACACAGGGCTCTGGTGGAGACTTTGTAGGTTAT 60
 QY 61 aagctgagcagagaggttatctgtgagctggcccccggggagggccagcagctgac 120
 Db 61 AAGCTGAGCAGAGGTTATCTGTGGAGCTGCCCGGGAGGGCCAGCAGCTGAC 120
 QY 121 ccgctgcacaaagccatggcggcagctggagatgagttcagagaccgcttcggcgacc 180
 Db 121 CCGCTGCACCAAGCCATGGCGCAGCTGGGAGATGAGTTTCGAGACCCGCTTCGGCGCACC 180
 QY 181 ttctctgatctggcggcagctgatgtgacccagcagctcagccagcagcagcttacc 240
 Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAGCTTCACC 240
 QY 241 caggctcccgacgaacttttcaaggggggcccaactggggccgctttagctctttt 300
 Db 241 CAGGCTCGATGACACTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 300
 QY 301 ctcttggggctgactgtgtgctgagagtgatcaacaaggagatggaaccactggtggga 360
 Db 301 GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
 QY 361 caagtgcaggaagtggcctacctgagagacggcggctggtgactggtatccacagc 420
 Db 361 CAAGTGCAGGAGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 420
 QY 421 agtggggcctggcggagttcaacagctctatacggggcggggccctggaggcggcgg 480
 Db 421 AGTGGGGCTGGCGGAGTGTCAACAGGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 480
 QY 481 cgtctgcggaggggaaactgggcatcagtgaggacagtgctgacggggcggcggcagctg 540
 Db 481 CGTCTGCGGAGGGAACTGGGCATCAGTGAGGACAGTGTCTGACGGGGCGGCTGGCACTG 540
 QY 541 ggggcccctgtaactgtaggggcctttttttagcaagt 581
 Db 541 GGGGGCCCTGGTAACGTAGGGGCCCTTTTGTCTAGCAAGT 581

RESULT 4
 V28334 standard; cDNA; 579 BP.
 AC V28334;
 DT 02-OCT-1998 (first entry)
 DE Human bcl-y gene.
 KW ss: bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
 OS Homo sapiens.
 FH key Location/Qualifiers
 FT CDS 1..579
 FT /*tag= a
 FT /product= bcl-y
 FT /note= "No stop codon given"
 PN US5789201-A.
 PD 04-AUG-1998.
 PF 11-FEB-1997; 798897.
 PR 23-FEB-1996; US-012201.
 PR 11-FEB-1997; US-798897.
 PA (COCE-) COGENSYS INC.
 PI Guastella J.
 DR WPI: 98-446079/38.
 DR P-PSDB; W61392.
 PT Nucleic acids encoding B-cell lymphoma-y protein - useful for

PT producing recombinant protein for use in treating uncontrolled cell
 growth e.g. cancers
 PS Claim 3; Column 15/16; 27pp; English.
 CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
 CC family, components in the cell death pathway. The bcl-2 family
 CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
 CC falls in the apoptosis activity category. The recombinant protein may
 CC be used to prevent uncontrolled cell growth, either by its direct
 CC administration to recombinant genetic constructs to increase its
 CC expression in vivo. Also, antisense constructs can be used in disorders
 CC where prevention of cell death is desired.
 SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T;

Query Match 97.4%; Score 567.8; DB 1; Length 579;
 Best Local Similarity 98.8%; Pred. No. 1.9e-131;
 Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 atggcagccagcctggcccccagacacacagcggctctgtgagcagactttgtaggttat 60
 Db 1 ATGGGACCCAGCCTGGGCCCCAGACACACAGGGCTCTGGTGGAGACTTTGTAGGTTAT 60
 QY 61 aagctgagcagagaggttatgtctgtgagctggcccccggggagggccagcagctgac 120
 Db 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGGCCAGCAGCTGAC 120
 QY 121 ccgctgcacaaagccatggcggcagctggagatgagttcagagaccgcttcggcgacc 180
 Db 121 CCACTGCACCAAGCCATGGCGGAGCTGGAGATGAGTTTCGAGAGCCCGCTTCCGGCGCACC 180
 QY 181 ttctctgatctggcggcagctgcatgtgacccagcagctcagccagcagcagcttacc 240
 Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAGCTTCACC 240
 QY 241 caggctcccgacgaacttttcaaggggggcccaactggggccgctttagctctttt 300
 Db 241 CAGGCTCCTGATGAACCTTTTCAAGGGGGGCCCAACTGGGGCGGCTTGTAGCTTCTTT 300
 QY 301 ctcttggggcctgactgtgtgagagtgatcaacaaggagatggaaccactggtggga 360
 Db 301 GTCTTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
 QY 361 caagtgcaggaagtggatggctgacctgagacggcggctgctgactggtatccacagc 420
 Db 361 CAAGTGCAGGAGTGGATGGTGGCTACCTCGAGAGCGCGCTGCTGACTGATCCACAGC 420
 QY 421 agtggggcctggcggagtgatcaacagctctatacggggacggggccctggaggcggcgg 480
 Db 421 AGTGGGGCTGGCGGAGTGTCAACAGCTCTATAGGAGACAGTGTCTGACGGGGCGGCTGGCACTG 480
 QY 481 cgtctgcggaggggaaactgggcatcagtgaggacagtgctgacggggcggcggcagctg 540
 Db 481 CGTCTGCGGAGGGAACTGGGCATCAGTGAGGACAGTGTCTGACGGGGCGGCTGGCACTG 540
 QY 541 ggggcccctgtaactgtaggggcctttttttagcaagt 579
 Db 541 GGGGCCCTGGTAACGTAGGGGCCCTTTTGTCTAGCAAG 579

RESULT 5
 X15946 standard; cDNA; 579 BP.
 AC X15946;
 DT 20-MAY-1999 (first entry)
 DE cDNA encoding the human bcl-y protein.
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; span;
 KW premature cell death; cell death stimulator; prolonged cell life length;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite; ss.

Db 181 TTCTGATCTGGCGGCTCAGTCGATGTCAGCCAGGCTCAGCCAGCAAGCTTCACC 240
 QY 241 caggtctccgacgaactttttcaaggggggcccccacactggggccgctttagccttttt 300
 Db 241 CAGGCTCCGACGAACATTTTCAAGGGGGCCCCAACCTGGGGCCGCTTGTAGCCCTCTTT 300
 QY 301 ctcttggggtgactgtgctgagagtgctcaacaaggagatggaaccactggtggga 360
 Db 301 CTCCTTGGGGCTGCACTGTGCTGAGAGTGTCAACAAGAGATGGAAACCACTGGTGGGA 360
 QY 361 caatgcaggagtgatggtggcctacctgagacgagcggtggtgcactggtatccacagc 420
 Db 361 CAAAGTCAGGAGTGGATGCTGCGCTACCTGGAGACGCGGCTGCTGCACTGGATCCACAGC 420
 QY 421 agtggggctggcgaggtcacagctctatacggggagacggggcccttgagagagcgcg 480
 Db 421 AGTGGGGCTGGCGGAGTTCAACGCTCTATACGGGGAGCGGGGCCCTGGAGAGCGCGG 480
 QY 481 cgtctcgggagggaaactgggcatcagtgaggacagtgtgacggggcggtggcactg 540
 Db 481 CGTCTGCGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGGTGGCACTG 540
 QY 541 ggggcccctgtaactgtgagggcccttttttctagcaagtga 583
 Db 541 GGGGCCCTGGTAACGTAGGGGCGCTTTTGTCTAGCAAGTGAA 583

RESULT 2

X25134
 ID X25134 standard; DNA; 583 BP.
 AC X25134;
 DT 05-JUL-1999 (first entry)
 DE Human bcl-w gene derivative.
 KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
 KW animal model; ss.
 OS Homo sapiens.
 PN WO9913710-A1.
 PD 25-MAR-1999.
 PR 16-SEP-1998; AU0764.
 PR 16-SEP-1997; AU-009228.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
 DR WPI; 99-243890/20.
 DR P-PSDB; Y05532.
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 protein associated with Bcl-w
 PS Disclosure: Page 36; 52pp; English.
 CC The present sequence is described as a derivative of the human
 CC Bcl-w gene (see X25132) and encodes Bcl-w protein (see Y05532), a
 CC pro-survival member of the Bcl-2 family which is widely expressed
 CC and which is essential for spermatogenesis. The invention relates
 CC generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for
 CC inducing or reducing fertility of male animals. Methods are
 CC provided for the treatment of infertility, or for reducing
 CC fertility, by modulating spermatogenesis. An animal model carries
 CC a mutation is at least one allele of the human or murine bcl-w gene
 CC or in a gene associated with bcl-w. Such animals have disorganised
 CC seminiferous tubules and are substantially infertile, but possess no
 CC other major abnormalities as determined by histological examination.
 CC They can be used to screen for therapeutic molecules including
 CC genetic sequences capable of inducing, enhancing or otherwise
 CC facilitating spermatogenesis in animals, or which can induce
 CC infertility.
 SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T;

Query Match 100.0%; Score 583; DB 1; Length 583;
 Best Local Similarity 100.0%; Pred. No. 3.5e-135;
 Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggagacccagctcgcccccagacacacagcggtctgtggcagacttttaggttat 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 ATGGCAGCCCGGCGCTCGGCCCGCCAGACACACAGGGCTCTGGTGGCACTTTGTAGTTAT 60
 QY 61 aaactagcagaaggtttatgtctgtgagctgccccggggagggcccaagcagctgac 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 AAGCTGAGGAGCAAGGGTTATGTCGTGAGCTGGCCCCGGGAGGGCCACACACTGAC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 ccgctgcacccaagccatgctgggagctgggagctgagttcgagaccccgcttcggcgacc 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 CCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTCCAGACCCGCTTCGCGGCACC 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 ttctctgatctggcgctcagctgcatgtgaccccaaggctcagccagaaagcttcacc 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 TTCTCTGATCTGGCGGCTCAGCTGTCATGTGACCCAGGCTCAGCCAGCAAGCTTCACC 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 caggtctccagaaactttttcaaggggggccccaactggggcgctttagccttttt 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 CAGGTCTCCGACGAACATTTTCAAGGGGGCCCCAACTGGGGCGGCTTGTAGCCTTCITT 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 ctcttggggctgacactgtgctgagagtgctcaacaaggagatggaaccactggtggga 360
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 Db 301 CTCTTTGGGGCTGCACTGTGCTGAGAGTGTCAACAAGAGATGGAAACCACTGGTGGGA 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 caagtgcaggagtgatggtggcctacctgagacgagcggtggtgcactggatccacagc 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 CAAAGTCAGGAGTGGATGCTGCGCTACCTGGAGACGCGGCTGCTGCACTGGATCCACAGC 420
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 QY 421 agtggggctggcgaggtcacagctctatacggggagacggggcccttgagagagcgcg 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 AGTGGGGCTGGCGGAGTTCAACGCTCTATACGGGGAGCGGGGCCCTGGAGAGCGCGG 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 481 cgtctcgggagggaaactgggcatcagtgaggacagtgtgacggggcggtggcactg 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 CGTCTGCGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGGTGGCACTG 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 541 ggggcccctgtaactgtgagggcccttttttctagcaagtga 583
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 GGGGCCCTGGTAACGTAGGGGCGCTTTTGTCTAGCAAGTGAA 583
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 3

X25132
 ID X25132 standard; DNA; 581 BP.
 AC X25132;
 DT 05-JUL-1999 (first entry)
 DE Human bcl-w gene.
 KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
 KW animal model; ss.
 OS Homo sapiens.
 PN WO9913710-A1.
 PD 25-MAR-1999.
 PR 16-SEP-1998; AU0764.
 PR 16-SEP-1997; AU-009228.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
 DR WPI; 99-243890/20.
 DR P-PSDB; Y05530.
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 protein associated with Bcl-w
 PS Claim 3; Page 32; 52pp; English.
 CC The present sequence is the human bcl-w gene encoding Bcl-w protein
 CC which is a member of the Bcl-2 family which is
 CC widely expressed and which is essential for spermatogenesis. The
 CC invention relates generally to a method of treatment and to an
 CC animal model for the identification of molecules and genetic
 CC sequences useful for inducing or reducing fertility of male
 CC animals. Methods are provided for the treatment of infertility, or
 CC for reducing fertility, by modulating spermatogenesis. An animal
 CC model carries a mutation is at least one allele of the human or
 CC murine bcl-w gene or in a gene associated with bcl-w. Such animals
 CC have disorganised seminiferous tubules and are substantially
 CC infertile, but possess no other major abnormalities as determined
 CC by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of

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OM nucleic - nucleic search, using sw model

Run on: July 3, 2000, 21:21:53 ; Search time 115.05 seconds
(without alignments)
1267.814 Million cell updates/sec

Title: US-09-155-327B-6

Perfect score: 583

Sequence: 1 atggcgacccagctcgcc.....ctttttgtcagcaagtga 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	583	100.0	583	1 T96577	Human bcl-w DNA. N
2	583	100.0	583	1 X25134	Human bcl-w gene d
3	573	98.3	581	1 X25132	Human bcl-w gene.
4	567.8	97.4	579	1 V28334	Human bcl-y gene.
5	567.8	97.4	579	1 X15946	cDNA encoding the
6	523	89.7	579	1 V28333	Rat bcl-y gene. Nu
7	523	89.7	579	1 X15945	cDNA encoding the
8	521.8	89.5	581	1 X25133	Mouse bcl-w gene.
9	501	85.9	581	1 T96578	Mouse bcl-w DNA. N
10	501	85.9	581	1 X25135	Mouse bcl-w gene d
11	424	72.7	1098	1 V41925	Nucleotide sequenc
12	423.6	72.7	1864	1 V59630	Human secreted pro
13	131	22.5	926	1 Q81698	Human thymus BCL-X
14	131	22.5	926	1 T40079	Bcl-XL gene. Induc
15	131	22.5	7372	1 X33182	Base sequence of t
16	123.4	21.2	765	1 Q49815	Bcl-2. Treating tu
17	123.4	21.2	953	1 X33183	Bcl-2 DNA fragment
18	123.4	21.2	5086	1 Q54631	Human oncogene bcl
19	123.4	21.2	5086	1 Q86661	Human bcl-2 gene.
20	123.4	21.2	5105	1 N81292	Sequence of bcl-2
21	123.4	21.2	7996	1 X33184	Base sequence of t
22	121.8	20.9	760	1 T33694	Human BCL2 cDNA. S
23	120.4	20.7	1384	1 V17638	Mouse BCL-x gamma
24	119	20.4	615	1 Q73987	Human bcl-2 gene O
25	119	20.4	911	1 X08431	bcl-2 proto-oncoge
26	115.8	19.9	831	1 N81293	Sequence of bcl-2
27	113.8	19.5	1274	1 Q81696	Chicken lymphoid B
28	52.6	9.0	737	1 Q81699	Human thymus BCL-X
29	52.2	9.0	822	1 T48488	Bax Omega protein
30	51.8	8.9	624	1 Q97605	Human Bax protein
31	51.8	8.9	624	1 V84005	cDNA encoding a hu
32	45.6	7.8	509	1 V89057	EST clone CB239. N
33	44.4	7.6	5408	1 Q95494	Human Cdn-3 DNA. N
34	44	7.5	114955	1 X53491	Human adenosine A1

ALIGNMENTS

RESULT 1

T96577
ID T96577 standard; DNA; 583 BP.
AC T96577;
DT 22-APR-1998 (first entry)
DE Human bcl-w DNA.
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..582
FT /tag= a
FT /product= bcl-w
FN W09735971-A1.
PD 02-OCT-1997.
PF 27-MAR-1997; AU0199.
PR 27-MAR-1996; AU-008965.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Adams JM, Cory S, Gibson LM, Holmgren SP;
DR WPI; 97-489635/45.
DR P-PSDB; W36047.
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
or inhibit cell survival, e.g. for treatment of cancer and
degenerative diseases
FS Claim 3; Page 48; 86pp; English.
CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
family, extracted from an adult brain library. This gene promotes cell
survival, so its modulation is useful in treatment of cancer or
auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
human immunodeficiency virus infection or in cell transplants.
CC Up-regulation of the gene can also be used to modify cell lines cultured
in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
and to increase survival of primary explants during genetic modification.
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
antibody production or screening of potential modulators.
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T;

Query Match 100.0%; Score 583; DB 1; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.5e-135;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atggcgacccagcctcgccgacacacacgagctctgtggtggcagactttaggttat 60
|||||
Db 1 ATGGCGACCCAGCCTCGGCCAGACACACAGCGGCTCTGTGGCAGACTTTAGGTTAT 60
Qy 61 aagctgggagaaagggttatgtctgtggagctgccccggggagggccagcagctgac 120
|||||
Db 61 AAGCTGGGAGAAAGGTTATGTCTGTGGAGCTGCCCGGGAGGGCCAGCAGCTGAC 120
Qy 121 ccgctgcaccaagccatgcggcagctggagatgagttcagacccgcttccgcgccacc 180
|||||
Db 121 CCGCTGCACCAAGCCATCGGGCGAGCTGGAGATGAGTTCGAGACCCCTTCCGCGCCACC 180
Qy 181 ttctctgatctggcggtcagctgcatgtgacccaggtcagcccgagcaacgttcaacc 240
|||||

Type III procollag
Vector pAC3A1 cont
HSV-2 strain SB5 C
HSV-2 strain SB5 C
Genomic clone G11F
Human thyroid tran
HSV-2 strain SB5 C
Human LDL receptor
Immunoglobulin D-r
Bak-2 gene. Screen
Human Cdn-2 DNA. N

35 40 6.9 3690 1 Q30849
36 40 6.9 5460 1 T16508
c 37 38 6.5 3004 1 V62162
c 38 38 6.5 117213 1 V62176
39 37.8 6.5 1505 1 Q55750
40 37.8 6.5 3293 1 T05810
41 37.2 6.4 4289 1 V62147
42 37 6.3 6843 1 T84509
43 37 6.3 14928 1 Q11707
44 36 6.2 1286 1 T42139
45 36 6.2 6511 1 Q95493

CC which tissues they are most highly expressed in (see V59511 for described
CC uses).
CC Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 0;

Query Match 62.7%; Score 364.4; DB 1; Length 1864;
Best Local Similarity 90.0%; Pred. No. 7.6e-89;
Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;
Qy 1 atgcgacccagcctcaacccagacacagcgctagtgctgacttgtagctat 60
Db 11 ATGCGACCCAGCCTCGGCCAGACACACAGCGCTCTGCTGCAGACTTTGTAGTTAT 70
Qy 61 aggtgagggcagaagggtatgtctgtgagctggcgctggggaagccagccgcgac 120
Db 71 AAGCTGAGGCGAGAGGCTTATGCTGTGGAGCTGGCCCCGGGAGGCCAGCAGCTGAC 130
Qy 121 ccgtgcacaaagccatgcggctgtgagagagttgagaccctgttcccgccacc 180
Db 131 CCGCTGACCAAGCATGCGGCGAGCKGAGATGAGTTTCGAGACCCGCTTCCGGCGCAC 190
Qy 181 ttctgacacgtccgtacgtacagtgacccaggtcagccagcaagcttcacc 240
Db 191 TTCTGTATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACACGCTTCACC 250
Qy 241 caggtttccgacgaactttccaaaggggccctaaactggggccgtctgtggcattctt 300
Db 251 CAGGTCTCCGATGACATTTTAAAGGGGGCCCCAACTGGGGCGCTTGTAGCTTCTTT 310
Qy 301 gtcttggggctccctgtgtgtgagagtgatcaacaaagaaatggagcccttgggtgga 360
Db 311 GTCTTTGGGCTCAGCTGTGTGTGAGAGTGTCAACAAGAGAGATGGAACCACTGGTGGGA 370
Qy 361 caagtcagagatggatcggtcctaccctgagacagctcgtgactggatccacagc 420
Db 371 CAAGTCAGGAGTGGATGGTGGCTCCTCTGAGACGCGGCTGCTGACTGGATCCACAGC 430
Qy 421 agtggcgctgg 432
Db 431 AGTGGGGCTGG 442

RESULT 13

Q81698
ID Q81698 standard; DNA; 926 BP.
AC Q81698;
DT 10-AUG-1995 (first entry)
DE Human thymus Bcl-XL DNA.
KW Bcl-XL; apoptosis; cell death; cancer; neurodegenerative disease;
KW autoimmune disease; Parkinson disease; amyotrophic lateral sclerosis;
KW multiple sclerosis; ss.
OS Homo sapiens.
PH Key
FT Location/Qualifiers
FT cds
FT 135..836
FT /*tag= a
FN W09500642-A.
PD 05-JAN-1995.
PF 22-JUN-1994; U07089.
PR 22-JUN-1993; US-081448.
PA (ARCH-) ARCH DEV CORP.
PA (UNMI) UNIV MICHIGAN.
PI Boise LH, Nunez G, Thompson CB;
DR WPI: 95-052079/07.
DR P-PSDB: R6887.
PT New poly-nucleotide encoding new poly-peptide(s) that modify
PT apoptosis - and related vectors, recombinant cells and
PT antibodies, useful in assay and for control of cell death in e.g.
PT neuronal cells, lymphocytes and cancers
PS Claim 5; Page 94; 127pp; English.
CC This DNA may be expressed recombinantly for the production of a BCL-
CC x protein, particularly with pcmv plasmids as vectors for
CC expression in mammalian cell cultures. The protein has particular
CC application in cancer cells (failure of programmed cell death (PCD))

CC or neurodegenerative and autoimmune diseases (premature PCD), e.g.
CC Parkinson's disease, amyotrophic lateral sclerosis and multiple
CC sclerosis.
CC Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0;

Query Match 23.2%; Score 134.6; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.6e-27;
Matches 236; Conservative 0; Mismatches 166; Indels 0; Gaps 0;
Qy 128 accaagcaatcggtgctgagagagtgagacccgtttccgcccgcacaccttctgt 187
Db 394 AGCAAGCGCTGAGGAGGAGCGAGCGAGTTTGAACCTGCGGTACCGGGGCAATTCAGTG 453
Qy 188 acctggcgctcagctacagctgacccaggtcagccagcaagcgttcccccaggtt 247
Db 454 ACCTGACATCCAGCTCCACATCACCCAGGAGACATATCAGAGCTTTGAACAGTAG 513
Qy 248 ccgacgaactttccaaaggggccctaaactggggtgagagcttgggtggacaagtc 367
Db 514 TGAATGAACCTCTTCGGGATGGGGTAAACTGGGTGCGCATTTGTCCTTCG 573
Qy 308 gggctgacctgtgtgagagtgatcaacaaagaaatggagcccttgggtggacaagtc 367
Db 574 GCGGGGCACTGTGCGTGAAGAGGTAGACAAGGAGATGCAGGTATTGCTGAGTCGATCG 633
Qy 368 agatttgatcggtcctacctggagacacgtctgtgctgagatccacagcagtgagc 427
Db 634 CAGCTTGGATGCCACTTACCTGAATGACCCTAGAGCCTTGGATCCAGGAGACGCGC 693
Qy 428 gctggcgagacttcacgtctctacgggagcggtgagcagcagcggtcgtctgc 487
Db 694 GCTGGGATACTTTTGTGGAACCTCTATGGAGCAATGTCAGACAGCCGAGAGGCC 753
Qy 488 gggagggcaactgggcatgagtgagcacacagtggtgacggggggcg 532
Db 754 AGGAAGCTTCAACCGCTGGTTCCTGACGGGCGATGACTGTGCGCG 798

RESULT 14

T40079
ID T40079 standard; cDNA; 926 BP.
AC T40079;
DT 30-MAR-1997 (first entry)
DE Bcl-XL gene.
KW Human; Bcl-XL; T-lymphocyte; cell death; gene therapy; HIV; AIDS;
KW antisense; immune disorder; autoimmune disease; graft rejection;
KW graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
OS Homo sapiens.
PH Key
FT Location/Qualifiers
FT cds
FT 135..836
FT /*tag= a
FT /product= Human bcl-XL protein
FN W09634956-A1.
PD 07-NOV-1996.
PF 02-MAY-1996; U06203.
PR 04-MAY-1995; US-435518.
PR 07-JUN-1995; US-481739.
PA (ARCH-) ARCH DEV CORP.
PA (USNA) US SEC OF NAVY.
PI June CH, Thompson CB;
DR WPI: 96-506159/50.
DR P-PSDB: W05821.
PT Inducing or preventing death of T cells by bcl-XL protein regulation
PT - used to increase survival of HIV infected cells or to
PT down-regulate immune responses in immune diseases
PS Disclosure; Page 51-52; 76pp; English.
CC This sequence encodes human bcl-XL protein, which protects
CC T-lymphocytes against cell death. The genomic bcl-X gene may
CC produce 2 different mRNAs, one encoding a long form (bcl-XL), the
CC other a short form (bcl-XS), lacking a stretch of 63 amino acids,
CC by differential splicing of the 2nd coding exon to a more proximal
CC 5'-splice donor within the 1st coding exon. Bcl-XS acts as a

Qy 421 agtgcgcgtgg 432
|||||
Db 421 AGTGGGGCTGG 432

RESULT 12
V59630
ID V59630 standard; DNA; 1864 BP.
AC V59630; 1999 (first entry)
DE Human secreted protein gene 120 clone HGBGZ64.
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN W0983948-A2.
PD 11-SEP-1998. U04493.
PF 06-MAR-1998; US-061060.
PR 02-OCT-1997; US-038621.
PR 07-MAR-1997; US-040161.
PR 07-MAR-1997; US-040162.
PR 07-MAR-1997; US-040163.
PR 07-MAR-1997; US-040333.
PR 07-MAR-1997; US-040334.
PR 07-MAR-1997; US-040336.
PR 07-MAR-1997; US-040626.
PR 11-APR-1997; US-043311.
PR 11-APR-1997; US-043312.
PR 11-APR-1997; US-043313.
PR 11-APR-1997; US-043314.
PR 11-APR-1997; US-043568.
PR 11-APR-1997; US-043569.
PR 11-APR-1997; US-043576.
PR 11-APR-1997; US-043578.
PR 11-APR-1997; US-043580.
PR 11-APR-1997; US-043669.
PR 11-APR-1997; US-043670.
PR 11-APR-1997; US-043671.
PR 11-APR-1997; US-043672.
PR 11-APR-1997; US-043674.
PR 23-MAY-1997; US-047492.
PR 23-MAY-1997; US-047500.
PR 23-MAY-1997; US-047501.
PR 23-MAY-1997; US-047502.
PR 23-MAY-1997; US-047503.
PR 23-MAY-1997; US-047581.
PR 23-MAY-1997; US-047582.
PR 23-MAY-1997; US-047583.
PR 23-MAY-1997; US-047584.
PR 23-MAY-1997; US-047585.
PR 23-MAY-1997; US-047586.
PR 23-MAY-1997; US-047587.
PR 23-MAY-1997; US-047588.
PR 23-MAY-1997; US-047589.
PR 23-MAY-1997; US-047590.
PR 23-MAY-1997; US-047592.
PR 23-MAY-1997; US-047593.
PR 23-MAY-1997; US-047594.
PR 23-MAY-1997; US-047595.
PR 23-MAY-1997; US-047596.
PR 23-MAY-1997; US-047597.
PR 23-MAY-1997; US-047598.
PR 23-MAY-1997; US-047599.
PR 23-MAY-1997; US-047600.
PR 23-MAY-1997; US-047601.
PR 23-MAY-1997; US-047612.
PR 23-MAY-1997; US-047613.

PR 23-MAY-1997; US-047614.
PR 23-MAY-1997; US-047615.
PR 23-MAY-1997; US-047617.
PR 23-MAY-1997; US-047618.
PR 23-MAY-1997; US-047632.
PR 23-MAY-1997; US-047633.
PR 06-JUN-1997; US-048964.
PR 06-JUN-1997; US-048974.
PR 13-JUN-1997; US-049610.
PR 08-JUL-1997; US-051926.
PR 16-JUL-1997; US-052874.
PR 18-AUG-1997; US-055724.
PR 22-AUG-1997; US-056630.
PR 22-AUG-1997; US-056631.
PR 22-AUG-1997; US-056632.
PR 22-AUG-1997; US-056636.
PR 22-AUG-1997; US-056637.
PR 22-AUG-1997; US-056662.
PR 22-AUG-1997; US-056664.
PR 22-AUG-1997; US-056845.
PR 22-AUG-1997; US-056862.
PR 22-AUG-1997; US-056864.
PR 22-AUG-1997; US-056872.
PR 22-AUG-1997; US-056874.
PR 22-AUG-1997; US-056875.
PR 22-AUG-1997; US-056876.
PR 22-AUG-1997; US-056877.
PR 22-AUG-1997; US-056878.
PR 22-AUG-1997; US-056879.
PR 22-AUG-1997; US-056880.
PR 22-AUG-1997; US-056881.
PR 22-AUG-1997; US-056882.
PR 22-AUG-1997; US-056884.
PR 22-AUG-1997; US-056886.
PR 22-AUG-1997; US-056887.
PR 22-AUG-1997; US-056888.
PR 22-AUG-1997; US-056889.
PR 22-AUG-1997; US-056892.
PR 22-AUG-1997; US-056893.
PR 22-AUG-1997; US-056894.
PR 22-AUG-1997; US-056903.
PR 22-AUG-1997; US-056908.
PR 22-AUG-1997; US-056909.
PR 22-AUG-1997; US-056910.
PR 22-AUG-1997; US-056911.
PR 05-SEP-1997; US-057650.
PR 05-SEP-1997; US-057669.
PR 05-SEP-1997; US-057761.
PR 12-SEP-1997; US-058785.
PR (HUMA-) HUMAN GENOME SCI INC.
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
PI Peng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
PI Kyaw H, Lafleur DM, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
PI WPI; 98-506364/43.
DR P-PSDB; W74848.
DR New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS Claim 1; Page 353-354; 721pp; English.
CC This sequence represents a nucleic acid molecule designated Gene 120 from
CC the human cDNA clone HGBGZ64 (deposited as clone ARCC 97902 and ARCC
CC 209048) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. V59502) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on

PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI: 99-214150/18.
DR P-PSDB; W97392.

PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
for modulating programmed cell death
PS Disclosure: Columns 15-16; 26pp; English.
CC The present sequence encodes human bcl-y protein (Rbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
CC bcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and bcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and bcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites. 111 T;
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T;

Query Match 85.6%; Score 497.4; DB 1; Length 579;
Best Local Similarity 91.2%; Pred. No. 1.2e-124;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 atgcgacccagcctcaacccagacacacgcgctctagtgtgctgactttgtagctat 60
DB 1 ATGGCCACCCCAAGCCTCGCGCCAGACACACGGGCTCTGGTGAAGACTTTTGTAGTTAT 60
QY 61 aggtgagcagaaggttatctgtgagctggcctggcctggcctggcctggcctggcct 120
DB 61 AAGCTGAGCAGAGAGGTTATGCTGTGGAGCTGGCCCGGGAGGGCCACAGCTGAC 120
QY 121 ccgctgaccacagcctcagcgtgctgagacagagtttgagacccgtttccgcgcacc 180
DB 121 CCAGTGCACCAAGCCATCGCGCAGCTGGAGATGAGTTGAGACCCGCTTCGCGCGCACC 180
QY 181 ttctctgactggcgtcagctacacgtgacccagcgtcagcgtcagcgtcagcgtcagc 240
DB 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAGCTTCACC 240
QY 241 caggtttccgacgaacttttccaaaggggcccctaactgggcccgtctgtgacattctt 300
DB 241 CAGGTCTCGATGAACCTTTTCAAGGGGGCCCACTGGGGCCGCTGTGAGCCCTTCATT 300
QY 301 gtctttgggctgcctgtgtgtgagagtgcaacaagaatgagcctttgttgga 360
DB 301 GTCTTTGGGGCTGCACTGTGTGTGTGAGAGTGTCACAAAGGAGATGAAACCTGTGGGA 360
QY 361 caagtccagattgattgctacgtacgtgagacacacgtcgtgctgactggtacacagc 420
DB 361 CAAGTGCAGGAGTGGATGGTGGCCCTACCTTGGAGAGCGCGGCTGGCTGATCCACAGC 420
QY 421 agtggcgctggcggaacttcaactctataggggagggggccctgagagcagcag 480
DB 421 AGTGGGGGCTGGCGGAGTTCACAGCTCTATACGGGGAGGGGGCCCTGGAGAGCGCGG 480
QY 481 cgtctgaggagggcaactgggcatgagtgagcagtggtgacgggggcccgtgagcagc 540
DB 481 CGTCTGCGGGAGGGNACTGGGCATCAGTGAGGACAGTGTCTGACGGGGCGCGTGCACTG 540
QY 541 ggggcccctgtaactgtaggggccctttttgtctagaag 579
DB 541 GGGGGCCCTGTAACCTGTAGGGGCCCTTTTGTGCTAGCAAG 579

RESULT 11

V41925
ID V41925 standard; cDNA; 1098 BP.
AC V41925;
DE 20-NOV-1998 (first entry)
DT Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
KW Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
KW immunological disorder; autoimmune disease; anti-infectious agent; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1098
FT /*tag= a
FT /product= "Bcl-like (HAICH29) protein"
PN W09831800-A2.
PD 23-JUL-1998.
PF 21-JAN-1998; U00960.
PR 21-JAN-1997; US-034205.
PR 21-JAN-1997; US-034204.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
PI Su JY;
DR WPI; 98-414099/35.
DR P-PSDB; W59884.
PT New isolated polynucleotides and encoded polypeptides - used to
PT develop products for treating e.g. inflammatory diseases,
PT infections, immunological disorders, autoimmune diseases, allergies
PT or tumours
PS Claim 2; Fig 12A-12D; 120pp; English.
CC This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
CC used in the method of the invention. The products of the clone can be
CC used for treating conditions associated with abnormal expression of
CC the polypeptides. They can be used for e.g. treating chronic
CC inflammatory diseases, immunological disorders, autoimmune diseases,
CC inflammatory diseases, various allergies, and as anti-infectious agents.
CC The products can also be used for detection and diagnosis.
SQ Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T;

Query Match 62.8%; Score 364.8; DB 1; Length 1098;
Best Local Similarity 90.3%; Pred. No. 5.2e-89;
Matches 390; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 atgcgacccagcctcaacccagacacacgcgctctagtgtgctgactttgtagctat 60
DB 1 ATGGCGACCCCAAGCCTCGCGCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
QY 61 aggtgagcagaaggttatctgtgagctggcctggcctggcctggcctggcctggcct 120
DB 61 AAGCTGAGCAGAGAGGTTATGCTGTGGAGCTGGCCCGGGAGGGCCACAGCTGAC 120
QY 121 ccgctgaccacagcctcagcgtgctgagacagagtttgagacccgtttccgcgcacc 180
DB 121 CCAGTGCACCAAGCCATCGCGCAGCTGGAGATGAGTTGAGACCCGCTTCGCGCGCACC 180
QY 181 ttctctgactggcgtcagctacacgtgacccagcgtcagcgtcagcgtcagcgtcagc 240
DB 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCAGGCTCAGCCCAACAGCTTCACC 240
QY 241 caggtttccgacgaacttttccaaaggggcccctaactgggcccgtctgtgacattctt 300
DB 241 CAGGTCTCGATGAACCTTTTCAAGGGGGCCCACTGGGGCCGCTGTGAGCCCTTCATT 300
QY 301 gtctttgggctgcctgtgtgtgagagtgcaacaagaatgagcctttgttgga 360
DB 301 GTCTTTGGGGCTGCACTGTGTGTGTGAGAGTGTCACAAAGGAGATGAAACCTGTGGGA 360
QY 361 caagtccagattgattgctacgtacgtgagacacacgtcgtgctgactggtacacagc 420
DB 361 CAAGTGCAGGAGTGGATGGTGGCCCTACCTTGGAGAGCGCGGCTGGCTGACTGATCCACAGC 420

Query Match	86.2%	Score 501;	DB 1;	Length 583;
Best Local Similarity	91.4%;	Pred. No. 1.3e-125;		
Matches 531;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	atgcacacccagcctcaacccagacacacgcgctagtggctagctagttagctat	60	
Db	1			
QY	61	aggctgaggcagaagggttatgtctgtgagctgggctgggaagcccgacgcgac	120	
Db	61			
QY	121	cgctgcacccaagccatcgggctgctgagacagagttgagacccgcttccgcgcacc	180	
Db	121			
QY	181	ttctctgacctggcgctcagctacacgtgaccccgagctcagccagcaacgtctcacc	240	
Db	181			
QY	241	caggtttccgacgaacttttccaagggggccctaaactggggccgtctgtggaattcttt	300	
Db	241			
QY	301	gtctttgggctgcacctgtgctgagagtgctcaacaaaataatgacgctttggcgga	360	
Db	301			
QY	361	caagtccaggaattgagctggcctacctcgagacacgtctggctgactggatccacagc	420	
Db	361			
QY	421	agtgcggctggcggaacttcaagctctaatacgggagcggggccctggaggacgcagcg	480	
Db	421			
QY	481	cgctctcgaggaggcaactgggcatgagtcagacagtgatgacgggggcccggcgacitg	540	
Db	481			
QY	541	ggggccctggtaactgtaggggccctttttgtcagcaagtg	581	
Db	541			

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RESULT      9
V28334
V28334 standard; cDNA; 579 BP.
ID          AC
V28334:
D2-OCT-1998 (first entry)
DE          Human bcl-1 gene.
KW          ss; bcl-1; bcl-2; cell death pathway; apoptotic; apoptosis; human.
OS          Homo sapiens.
FH          Key
FT          CDS
              Location/Qualifiers
              1..579
              /*tag= a
              /product= bcl-1
              /note= "No stop codon given"

US5789201-A.
04-AUG-1998.
PF          11-FEB-1997; 798897.
PR          23-FEB-1996; US-012201.
PR          11-FEB-1997; US-798897.
PA          (COCE-) COCENSYS INC.
PI          Guastella J;
DR          WPI; 98-446079/38.
P-PSDB; W61392.
PT          Nucleic acids encoding B-cell lymphoma-1 protein - useful for
producing recombinant protein for use in treating uncontrolled cell
growth e.g. cancers
PT          Claim 3; Column 15/16; 27pp; English.
PS          The mammalian bcl-1 genes encode a protein that is a member of the bcl-2
CC          family, components in the cell death pathway. The bcl-2 family
CC          family, components in the cell death pathway. The bcl-2 family

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CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontrolled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired. 111 T;
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T;

Query Match 85.6%; Score 497.4; DB 1; Length 579;
Best Local Similarity 91.2%; Pred. No. 1.2e-124;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 atgcgcacccagcctcaacccagacacacgcgcctctagtggctgactttgtaggtat 60
DB 1 ATGGGACCCACGCTCGGCCCCAGACACACGCGCTCTGGTGAAGACTTTGTAGGTAT 60

QY 61 agcgtgagcagaagggttatgtctgtgagctagggcctggggaagccacgcgcac 120
DB 61 AAGCTGAGGCGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120

QY 121 ccgctgcaccagccatcgggctgctgagacagattgagaccggtttccgcgcac 180
DB 121 CCACGTGCACCAAGCCATCGGGGACGTGGAGATGAGTTCGAGACCCGCTTCGGGGCGCAC 180

QY 181 ttctctgacctggccgtcagctacacgtgacccacaggtcagccacgacgcttcacc 240
DB 181 TTCTCTGATCTGGGGCTCAGCTGCATGTGACCCACGCTCAGCCCAACACGCTTCACC 240

QY 241 caggtttccgcagcaactttccagggggccctaacctgaggccgtctgttggaattctt 300
DB 241 CAGGTCCTCCGATGAACCTTTTCAAGGGGGCCCCAACCTGGGGCCGCTTGTAGCCCTTCTT 300

QY 301 gctcttggggctccctgtgctgaagtgctcaacaaagaaatggagccttggtgga 360
DB 301 GCTCTTGGGGCTGCACCTGTGCTGAGAGTGTCAACAGGAGATGGAAACCACTGGTGGA 360

QY 361 caagtccaggattggatcgtgctcactcgagacacgctcgtgctgactggatccacagc 420
DB 361 CAAGTGCAGGAGTGATGGTGGCTACCTCGAGACGGGCTGGCTGACTGGATCCACAGC 420

QY 421 agtgcgctggggcgacttcacagctctatacaggggaagggccctggaggaagcagcg 480
DB 421 AGTGGGGGCTGGGCGGAGTTTCACAGCTATACGGGGACGGGGGCGCTGGAGGAGCGCGG 480

QY 481 cgtctcgggagggcaactggcgcagtgagcacagtggtgacggggcgctggcactg 540
DB 481 CGTCTGCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGCTACGGGGCGCTGGCACTG 540

QY 541 ggggcccctgtaactgtaggggccttttttctagcaag 579
DB 541 GGGGCCCCGTGGTGAAGTGTAGGGGCCCTTTTTCGTAGCAAG 579

RESULT 10
X15946
ID X15946 standard; cDNA; 579 BP.
AC X15946;
DT 20-MAY-1999 (first entry)
DE cDNA encoding the human bcl-y protein.
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite; ss.
OS Homo sapiens.
PN US8683229-A.
PD 16-MAR-1999.
PR 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.

QY 301 gtcttggggtgcctgtgtgagagtgatgacacaaagaaatggagcctttgttggga 360
 |||||
 Db 301 GTCCTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGGAGATGGACCACTGGTGGGA 360
 |||||
 QY 361 caagtccaggattgagctgtgacctacacgtctgagacacgtctggtgactggtacacagc 420
 |||||
 Db 361 CAAGTGCAGGAGTGGATGGTGGCTACCTGAGAGACGGGCTGGCTGACTGGATCCACAGC 420
 |||||
 QY 421 agtggcgctgggcggagcttccacagctctacacgggacggggccctggagagcagcagc 480
 |||||
 Db 421 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
 |||||
 QY 481 cgtctgcggagggcaactggcagtgatgagacagtggtgacggggccgtgacactg 540
 |||||
 Db 481 CBTCTGCGGAGGGAAGTGGGCAFCAGTGAGGAGTGTCTGACGGGGCCGTGGCACTG 540
 |||||
 QY 541 ggggcccctgtaactgtaggggccctttttgtacgaagt 581
 |||||
 Db 541 GGGGCCCTGGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTG 581
 |||||

RESULT 7

T96577
 ID T96577 standard; DNA; 583 BP.
 AC T96577;
 DT 22-APR-1998 (first entry)
 DE Human bcl-w DNA.
 KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 diagnosis; degenerative disease; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..582
 FT /*tag= a
 FT /product= bcl-w
 PN WO9735971-A1.
 PD 02-OCT-1997.
 PF 27-MAR-1997; AU0199.
 PR 27-MAR-1996; AU-008965.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Adams JM, Cory S, Gibson LM, Holmgren SP;
 DR WPI; 97-489635/45.
 P-PSDB: W36047.
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
 or inhibit cell survival, e.g. for treatment of cancer and
 PT degenerative diseases
 PS Claim 3; Page 48; 86pp; English.
 CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
 family, extracted from an adult brain library. This gene promotes cell
 survival, so its modulation is useful in treatment of cancer or
 CC auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
 disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
 CC human immunodeficiency virus infection or in cell transplants.
 CC Up-regulation of the gene can also be used to modify cell lines cultured
 in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
 CC and to increase survival of primary explants during genetic modification.
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
 CC antibody production or screening of potential modulators.
 SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T;

Query Match 86.28; Score 501; DB 1; Length 583;
 Best Local Similarity 91.4; Pred. No. 1.3e-125;
 Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 1 atgcgcacccagctcaccacccagacacgcgcctctagtggctgactttgtaggctat 60
 |||
 Db 1 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTGTAGGTAT 60
 |||
 QY 61 aggtcagcgaaggggttatgtctgtgagctgggctgggagggccagccgcagc 120
 |||
 Db 61 AAGCTGAGGCAGAGAGGGTATGTCTGTGGAGCTGCCCGGGGAGGCCACGACGCTGAC 120
 |||

QY 121 ccgctgcaccacccatcggggctgagagcagagtttggagaccgcttccgcgcacc 180
 |||||
 Db 121 CCCTGCACCAACCCATCGGGCAGCTGGAGATGACTTCGAGACCCGCTTCGGGGCACC 180
 |||||
 QY 181 ttcttgacctggccgctcagctacacgtgacccccaggctcagccagcaagcttcacc 240
 |||||
 Db 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTACCCAGGCTCAGCCCAAGCAAGCTTCACC 240
 |||||
 QY 241 caggtttccgacgaacttttccaagggggccctaaactaactggggcgtttgtgcatcttt 300
 |||||
 Db 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCCAACTGGGGCGGCTTTGTAGCCTTCCTTT 300
 |||||
 QY 301 gtcttggggctccctgtgtgagagtgatcaacaaagaaatgagcctttgttgggga 360
 |||||
 Db 301 CTCTTTGGGCTGCATGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360
 |||||
 QY 361 caagtccaggattgagctgtgacctacacgtctgagacacgtctggtgactggatccacagc 420
 |||||
 Db 361 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 420
 |||||
 QY 421 agtggcgctgggcggagcttccacagctctacacgggacggggccctggagagcagcagc 480
 |||||
 Db 421 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGCGG 480
 |||||
 QY 481 cgtctgcggagggcaactggcagtgatgagacacagtggtgacggggccgtgagcactg 540
 |||||
 Db 481 CGTCTCGGGAGGGGAACTGGGCACTCAGTGAGGACAGTCTGACGGGGCCCTGGGCACTG 540
 |||||
 QY 541 ggggcccctgtaactgtaggggccctttttgtacgaagt 581
 |||||
 Db 541 GGGGCCCTGGTAACTGTAGGGGCCCTTTTGTCTAGCAAGTG 581
 |||||

RESULT 8

X25134
 ID X25134 standard; DNA; 583 BP.
 AC X25134;
 DT 05-JUL-1999 (first entry)
 DE Human bcl-w gene derivative.
 KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
 animal model; ss.
 OS Homo sapiens.
 PN WO913710-A1.
 PD 25-MAR-1999.
 PF 16-SEP-1998; AU0764.
 PR 16-SEP-1997; AU-009228.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
 DR WPI; 99-243890/20.
 P-PSDB: Y05532.
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w
 PS Disclosure; Page 36; 52pp; English.
 CC The present sequence is described as a derivative of the human
 CC bcl-w gene (see X25132) and encodes Bcl-w protein (see Y05532), a
 CC pro-survival member of the Bcl-2 family which is widely expressed
 CC and which is essential for spermatogenesis. The invention relates
 CC generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for
 CC inducing or reducing fertility of male animals. Methods are
 CC provided for the treatment of infertility, or for reducing
 CC fertility, by modulating spermatogenesis. An animal model carries
 CC a mutation is at least one allele of the human or murine bcl-w gene
 CC or in a gene associated with bcl-w. Such animals have disorganised
 CC seminiferous tubules and are substantially infertile, but possess no
 CC other major abnormalities as determined by histological examination.
 CC They can be used to screen for therapeutic molecules including
 CC genetic sequences capable of inducing, enhancing or otherwise
 CC facilitating spermatogenesis in animals, or which can induce
 CC infertility.
 SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T;

Result No.	Query			ID	Description
	Score	Match	Length		
1	581	100.0	581	1	Mouse bcl-w DNA. N
2	581	100.0	581	1	Mouse bcl-w gene d
3	560.2	96.4	581	1	Mouse bcl-w gene.
4	540.6	93.0	579	1	Rat bcl-y gene. Nu
5	540.6	93.0	579	1	cDNA encoding the
6	502.6	86.5	581	1	Human bcl-w gene.
7	501	86.2	583	1	Human bcl-w DNA. N
8	501	85.2	583	1	Human bcl-w gene d
9	497.4	85.6	579	1	Human bcl-y gene.
10	497.4	85.6	579	1	cDNA encoding the
11	364.8	62.8	1098	1	Nucleotide sequenc
12	364.4	62.7	1864	1	Human secreted pro
13	134.6	23.2	926	1	Human thymus BCL-X
14	134.6	23.2	926	1	Bcl-XL gene. Induc
15	134.6	23.2	7372	1	Base sequence of t
16	125	21.5	765	1	Bcl-2. Treating tu
17	125	21.5	953	1	Bcl-2 DNA fragment
18	125	21.5	5086	1	Human oncogene bcl
19	125	21.5	5086	1	Human bcl-2 gene.
20	125	21.5	5105	1	Sequence of bcl-2
21	125	21.5	7996	1	Base sequence of t
22	123.4	21.2	760	1	Human BCL2 cDNA. S
23	120.2	20.7	1274	1	Chicken lymphoid B
24	119	20.5	615	1	Human bcl-2 gene O
25	119	20.5	911	1	bcl-2 proto-oncoge
26	115.8	19.9	831	1	Sequence of bcl-2
27	113.8	19.6	1384	1	Mouse BCL-x gamma
28	57	9.8	737	1	Human thymus BCL-X
29	44.4	7.6	5408	1	Human Cdh-3 DNA. N
30	40.6	7.0	624	1	Human Bax protein
31	40.6	7.0	624	1	cDNA encoding a hu
32	39.4	6.8	822	1	Bax omega protein
33	37.6	6.5	1286	1	Bak-2 gene. Screen
34	37.6	6.5	6511	1	Human Cdh-2 DNA. N

QY 6I FSDLAAQLHVIFGSAQLKFIQVSDLEFQGGFNWGRVAFELFGARDCAESVKNEMLEFLVS 12

1000

PR 25-NOV-1997; US-978523.
 PA (COCE-) COCENSYS INC.
 PI Guastella J;
 DR WPI; 99-214150/18.
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
 PS for modulating programmed cell death
 CC Claim 2; Columns 19-22; 26pp; English.
 CC The present sequence represents a mammalian bcl-y protein.
 CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis- conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent.
 CC They may also be used in this way to develop cell lines which remain
 CC viable in culture for an extended period. In contrast, if they act as
 CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
 CC conditions associated with prolonged cell life span such as cancer
 CC (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
 CC diseases. They may also be used to cause cell death in, and hence
 CC control, parasites.
 SQ Sequence 192 AA;

Query Match 97.9%; Score 1368; DB 1; Length 192;
 Best Local Similarity 98.4%; Pred. No. 1.42e-120;
 Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 ATPASAPDTRALVDFVGYKLRQKGYVCGAGPGCGPAADPLHQAMRAAGDEFTFRRTF 60
 QY 2 ATPASAPDTRALVDFVGYKLRQKGYVCGAGPGCGPAADPLHQAMRAAGDEFTFRRTF 61
 Db 61 SDLAALQHLVTPGSAQQRFTQVSDQLFQGGPNWGRVLAFFVFGAALCAESVKNEMEPLVGQ 120
 QY 62 SDLAALQHLVTPGSAQQRFTQVSDQLFQGGPNWGRVLAFFVFGAALCAESVKNEMEPLVGQ 121
 Db 121 VQDMWVYLETPLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVALG 180
 QY 122 VQDMWVYLETPLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVALG 181
 Db 181 ALVTVGGAFFASK 192
 QY 182 ALVTVGGAFFASK 193

RESULT 10
 ID W97393 standard; Protein; 192 AA.
 AC W97393;
 DT 20-MAY-1999 (first entry)
 DE Protein sequence of the specification.
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite.
 OS Unidentified.
 PN US583229-A.
 PD 16-MAR-1999.
 PF 25-NOV-1997; 978523.
 PR 23-FEB-1996; US-012201.
 PR 11-FEB-1997; US-798897.
 PR 25-NOV-1997; US-978523.
 PA (COCE-) COCENSYS INC.
 PI Guastella J;
 DR WPI; 99-214150/18.
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful

PT for modulating programmed cell death
 PS Disclosure; Columns 19-20; 26pp; English.
 CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis- conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent.
 CC They may also be used in this way to develop cell lines which remain
 CC viable in culture for an extended period. In contrast, if they act as
 CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
 CC conditions associated with prolonged cell life span such as cancer
 CC (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
 CC diseases. They may also be used to cause cell death in, and hence
 CC control, parasites.
 SQ Sequence 192 AA;

Query Match 97.9%; Score 1367; DB 1; Length 192;
 Best Local Similarity 97.4%; Pred. No. 1.79e-120;
 Matches 187; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 1 ATPASTPDTRALVDFVGYKLRQKGYVCGAGPGCGPAADPLHQAMRAAGDEFTFRRTF 60
 QY 2 ATPASAPDTRALVDFVGYKLRQKGYVCGAGPGCGPAADPLHQAMRAAGDEFTFRRTF 61
 Db 61 SDLAALQHLVTPGSAQQRFTQVSDQLFQGGPNWGRVLAFFVFGAALCAESVKNEMEPLVGQ 120
 QY 62 SDLAALQHLVTPGSAQQRFTQVSDQLFQGGPNWGRVLAFFVFGAALCAESVKNEMEPLVGQ 121
 Db 121 VQDMWVYLETPLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVALG 180
 QY 122 VQDMWVYLETPLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVALG 181
 Db 181 ALVTVGGAFFASK 192
 QY 182 ALVTVGGAFFASK 193

RESULT 11
 ID Y05533 standard; Protein; 192 AA.
 AC Y05533;
 DT 05-JUL-1999 (first entry)
 DE Mouse Bcl-w protein derivative.
 KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 KW animal model.
 OS Mus sp.
 PN W09913710-A1.
 PD 25-MAR-1999.
 PF 16-SEP-1998; AU0764.
 PR 16-SEP-1997; AU-009228.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
 DR WPI; 99-243890/20.
 DR N-PSDB; X25135.
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w
 PS Disclosure; Page 39; 52pp; English.
 CC The present sequence is described of a derivative of mouse Bcl-w
 CC (see also Y05531), a pro-survival member of the Bcl-2 family that
 CC is widely expressed and which is essential for spermatogenesis.
 CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.
 CC The invention relates generally to a method of treatment and to an
 CC animal model for the identification of molecules and genetic
 CC sequences useful for inducing or reducing fertility of male animals.
 CC Methods are provided for the treatment of infertility, or for
 CC reducing fertility, by modulating spermatogenesis. An animal model
 CC carries a mutation in at least one allele of the human or murine
 CC bcl-w gene (see X25132-35) or in a gene associated with bcl-w.

QY 121 QVQEMVAYLETRLDVWIIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180
 DB 181 GALVTGGAFFASK 193
 QY 181 GALVTGGAFFASK 193
 RESULT 7
 ID W97391 standard; Protein; 193 AA.
 AC W97391;
 DT 20-MAY-1999 (first entry)
 DE The rat bcl-y protein.
 KW Rat bcl-y protein; Hbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite.
 OS Rattus sp.
 PN US5883229-A.
 PD 16-MAR-1999.
 PF 25-NOV-1997; 978523.
 PR 23-FEB-1996; US-012201.
 PR 11-FEB-1997; US-798897.
 PR 25-NOV-1997; US-978523.
 PA (COCE-) COCENSYS INC.
 PI Guastella J;
 DR WPI: 99-214150/18.
 DR N-PSDB: X15945.
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
 PT for modulating programmed cell death
 PS Disclosure; Columns 15-18; 26pp; English.
 CC The present sequence represents rat bcl-y protein (Hbcl-y). The
 CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
 CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's Disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral
 CC sclerosis; conditions where cells under go premature cell death as a
 CC result of triggers which may or may not be apparent. They may also be
 CC used in this way to develop cell lines which remain viable in culture for
 CC an extended period. In contrast, if they act as cell death stimulators,
 CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
 CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites.
 SQ Sequence 193 AA;

Query Match 98.6%; Score 1378; DB 1; Length 193;
 Best Local Similarity 97.4%; Pred. No. 1.46e-121;
 Matches 188; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 DB 1 MATPASTPTDTRALVADFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETFRRT 60
 QY 1 MATPASAPDTRALVADFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETFRRT 60
 DB 61 FSDLAQLHVTGSAQORFTQVSDLEFQGGPNWGRVLAFFVFGAALCAESVNKMEPLVG 120
 QY 61 FSDLAQLHVTGSAQORFTQVSDLEFQGGPNWGRVLAFFVFGAALCAESVNKMEPLVG 120
 DB 121 QVQEMVAYLETRLDVWIIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180
 QY 121 QVQEMVAYLETRLDVWIIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180
 DB 181 GALVTGGAFFASK 193
 QY 181 GALVTGGAFFASK 193
 RESULT 9
 ID W97394 standard; Protein; 192 AA.
 AC W97394;
 DT 20-MAY-1999 (first entry)
 DE Mammalian bcl-y protein.
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite.
 OS Mammalia.
 PN US5883229-A.
 PD 16-MAR-1999.
 PF 25-NOV-1997; 978523.
 PR 23-FEB-1996; US-012201.
 PR 11-FEB-1997; US-798897.

QY 181 GALVTGGAFFASK 193
 RESULT 8
 ID W61391 standard; Protein; 193 AA.
 AC W61391;
 DT 02-OCT-1998 (first entry)
 DE Rat bcl-y protein.
 KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
 OS Rattus sp.
 PN US5789201-A.
 PD 04-AUG-1998.
 PF 11-FEB-1997; 798897.
 PR 23-FEB-1996; US-012201.
 PR 11-FEB-1997; US-798897.
 PA (COCE-) COCENSYS INC.
 PI Guastella J;
 DR WPI: 98-446079/38.
 DR N-PSDB: V283333.
 PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
 PT producing recombinant protein for use in treating uncontrolled cell
 PT growth e.g. cancers
 PS Example; Fig 3A; 27pp; English.
 CC The mammalian bcl-y protein is a member of the bcl-2 family, components
 CC in the cell death pathway. The bcl-2 family have both apoptotic activity
 CC and the apoptosis blocking activity. bcl-y falls in the apoptosis
 CC activity category. The recombinant protein may be used to prevent
 CC uncontrolled cell growth, either by its direct administration to
 CC recombinant genetic constructs to increase its expression in vivo. Also,
 CC antisense constructs can be used in disorders where prevention of cell
 CC death is desired.
 SQ Sequence 193 AA;

Query Match 98.6%; Score 1378; DB 1; Length 193;
 Best Local Similarity 97.4%; Pred. No. 1.46e-121;
 Matches 188; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 DB 1 MATPASTPTDTRALVADFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETFRRT 60
 QY 1 MATPASAPDTRALVADFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETFRRT 60
 DB 61 FSDLAQLHVTGSAQORFTQVSDLEFQGGPNWGRVLAFFVFGAALCAESVNKMEPLVG 120
 QY 61 FSDLAQLHVTGSAQORFTQVSDLEFQGGPNWGRVLAFFVFGAALCAESVNKMEPLVG 120
 DB 121 QVQEMVAYLETRLDVWIIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180
 QY 121 QVQEMVAYLETRLDVWIIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180
 DB 181 GALVTGGAFFASK 193
 QY 181 GALVTGGAFFASK 193

CC molecules and genetic sequences useful for inducing or reducing
 CC fertility of male animals. Methods are provided for the treatment
 CC of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation is at least
 CC one allele of the human or murine bcl-2 gene (see X25132-35) or in
 CC a gene associated with bcl-2. Such animals have disorganised
 CC seminiferous tubules and are substantially infertile, but possess no
 CC other major abnormalities as determined by histological examination.
 CC They can be used to screen for therapeutic molecules including
 CC genetic sequences capable of inducing, enhancing or otherwise
 CC facilitating spermatogenesis in animals, or which can induce
 CC infertility.
 SQ Sequence 193 AA;

Query Match 98.8%; Score 1380; DB 1; Length 193;
 Best Local Similarity 97.9%; Pred. No. 9.23e-122;
 Matches 189; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 MATPASPTDTRALVDFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
 QY 1 MATPASPTDTRALVDFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
 Db 61 FSDLAALQHLVTPGSAOQRFTQVSDLFQGGPNWGRVAVFFVFGAALCAESVNKEMEPLVG 120
 QY 61 FSDLAALQHLVTPGSAOQRFTQVSDLFQGGPNWGRVAVFFVFGAALCAESVNKEMEPLVG 120
 Db 121 QVQEMVAYLETRLDWIHSSGGWAEFTALYGDGALEEARRLREGNWSVVRTLTGAVAL 180
 QY 121 QVQEMVAYLETRLDWIHSSGGWAEFTALYGDGALEEARRLREGNWSVVRTLTGAVAL 180
 Db 181 GALVTVGGAFFASK 193
 QY 181 GALVTVGGAFFASK 193

RESULT 5

ID W61392 standard; Protein; 193 AA.
 AC W61392;
 DT 02-OCT-1998 (first entry)
 DE Human bcl-2 protein.
 KW bcl-2; cell death pathway; apoptotic; apoptosis; human.
 OS Homo sapiens.
 PN US5789201-A.
 PD 04-AUG-1998.
 PF 11-FEB-1997; 798897.
 PR 23-FEB-1996; US-012201.
 PR 11-FEB-1997; US-798897.
 PA (COCE-) COCENSYS INC.
 PI Guastella J;
 DR WPI; 98-446079/38.
 DR N-PSDB; V28334.
 PT Nucleic acids encoding B-cell lymphoma-2 protein - useful for
 PT producing recombinant protein for use in treating uncontrolled cell
 PT growth e.g. cancers
 PS Example: Column 17/18; 27pp; English.
 CC The mammalian bcl-2 protein is a member of the bcl-2 family, components
 CC in the cell death pathway. The bcl-2 family have both apoptotic activity
 CC and the apoptosis blocking activity. bcl-2 falls in the apoptosis
 CC activity category. The recombinant protein may be used to prevent
 CC uncontrolled cell growth, either by its direct administration to
 CC recombinant genetic constructs to increase its expression in vivo. Also,
 CC antisense constructs can be used in disorders where prevention of cell
 CC death is desired.
 SQ Sequence 193 AA;

Query Match 98.7%; Score 1379; DB 1; Length 193;
 Best Local Similarity 98.4%; Pred. No. 1.16e-121;
 Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 MATPASPTDTRALVDFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
 QY 1 MATPASPTDTRALVDFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db 61 FSDLAALQHLVTPGSAOQRFTQVSDLFQGGPNWGRVAVFFVFGAALCAESVNKEMEPLVG 120
 QY 61 FSDLAALQHLVTPGSAOQRFTQVSDLFQGGPNWGRVAVFFVFGAALCAESVNKEMEPLVG 120
 Db 121 QVQEMVAYLETRLDWIHSSGGWAEFTALYGDGALEEARRLREGNWSVVRTLTGAVAL 180
 QY 121 QVQEMVAYLETRLDWIHSSGGWAEFTALYGDGALEEARRLREGNWSVVRTLTGAVAL 180
 Db 181 GALVTVGGAFFASK 193
 QY 181 GALVTVGGAFFASK 193

RESULT 6

ID W97392 standard; Protein; 193 AA.
 AC W97392;
 DT 20-MAY-1999 (first entry)
 DE The human bcl-2 protein.
 KW Rat bcl-2 protein; Rbcl-2; human bcl-2 protein; Hbcl-2; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite.
 OS Homo sapiens.
 PN US5883229-A.
 PD 16-MAR-1999.
 PF 25-NOV-1997; 978523.
 PR 23-FEB-1996; US-012201.
 PR 11-FEB-1997; US-798897.
 PR 25-NOV-1997; US-978523.
 PA (COCE-) COCENSYS INC.
 PI Guastella J;
 DR WPI; 99-214150/18.
 DR N-PSDB; X15946.
 PT Novel bcl-2 homologues of the rat and human bcl-2 protein - useful
 PT for modulating programmed cell death
 PS Claim 1; Columns 17-18; 26pp; English.
 CC The present sequence represents human bcl-2 protein (Hbcl-2). The
 CC specification also describes rat bcl-2 protein (Rbcl-2). Rbcl-2 and
 CC Hbcl-2 are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's Disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral
 CC sclerosis- conditions where cells under go premature cell death as a
 CC result of triggers which may or may not be apparent. They may also be
 CC used in this way to develop cell lines which remain viable in culture for
 CC an extended period. In contrast, if they act as cell death stimulators,
 CC Rbcl-2 and Hbcl-2 may be used to treat conditions associated with
 CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites.

Query Match 98.7%; Score 1379; DB 1; Length 193;
 Best Local Similarity 98.4%; Pred. No. 1.16e-121;
 Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 MATPASPTDTRALVDFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
 QY 1 MATPASPTDTRALVDFVGYKLRQGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60
 Db 61 FSDLAALQHLVTPGSAOQRFTQVSDLFQGGPNWGRVAVFFVFGAALCAESVNKEMEPLVG 120
 QY 61 FSDLAALQHLVTPGSAOQRFTQVSDLFQGGPNWGRVAVFFVFGAALCAESVNKEMEPLVG 120
 Db 121 QVQEMVAYLETRLDWIHSSGGWAEFTALYGDGALEEARRLREGNWSVVRTLTGAVAL 180

QY 61 FSDLAQLHVTGSAQQRFTQVSDLELFGQGNWGRVAVFFLFGAALCAESVKNEMEPLVG 120

Db 121 QVQEMWVAYLETRLDVWIIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 QVQEMWVAYLETRLDVWIIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 181 GALVTGGAFFASK 193
 ||||||||||||||||

QY 181 GALVTGGAFFASK 193

RESULT 2

ID W36047 standard; Protein; 193 AA.

AC W36047; 1998 (first entry)

DT 22-APR-1998 (first entry)

DE Human bcl-w protein.

KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;

KW diagnosis; degenerative disease.

OS Homo sapiens.

PN W05735971-A1.

PD 02-OCT-1997.

PF 27-MAR-1997; AU0199.

PR 27-MAR-1996; AU-008965.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Adams JM, Cory S, Gibson LM, Holmgren SP;

DR WPI: 97-489635/45.

DR N-PSDB; T96577.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce

PT or inhibit cell survival, e.g. for treatment of cancer and

PT degenerative diseases

PS Claim 6; Page 48; 86pp; English.

CC This sequence represents a novel human protein, bcl-w, encoded by the

CC bcl-2 gene family and extracted from an adult brain library. This gene

CC promotes cell survival, so its modulation is useful in treatment of

CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,

CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,

CC ischaemia, human immunodeficiency virus infection or in cell transplants.

CC Up-regulation of the gene can also be used to modify cell lines cultured

CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas

CC and to increase survival of primary explants during genetic modification.

CC It can be used to produce recombinant bcl-w for therapy, diagnosis,

CC antibody production or screening of potential modulators.

CC Sequence 193 AA;

QY Query Match 100.0%; Score 1397; DB 1; Length 193;

Best Local Similarity 100.0%; Pred. No. 1.91e-123;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATPASAPDTRALVADFGYKLRQGYVCGAGPGEGPAADPLHQAMRAAGDEFFETFRRT 60
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QY 1 MATPASAPDTRALVADFGYKLRQGYVCGAGPGEGPAADPLHQAMRAAGDEFFETFRRT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 61 FSDLAQLHVTGSAQQRFTQVSDLELFGQGNWGRVAVFFLFGAALCAESVKNEMEPLVG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 FSDLAQLHVTGSAQQRFTQVSDLELFGQGNWGRVAVFFLFGAALCAESVKNEMEPLVG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 121 QVQEMWVAYLETRLDVWIIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 QVQEMWVAYLETRLDVWIIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 181 GALVTGGAFFASK 193

QY 181 GALVTGGAFFASK 193

RESULT 3

ID Y05530 standard; Protein; 193 AA.

AC Y05530;

DT 05-JUL-1999 (first entry)

DE Human Bcl-w protein essential for spermatogenesis.

KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;

KW animal model.

OS Homo sapiens.

PN W09913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; AU0764.

PR 16-SEP-1997; AU-009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Adams J, Cory S, Gibson L, Koentgen F, Print C;

DR WPI: 99-243890/20.

DR N-PSDB; X25132.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

PT protein associated with Bcl-w

PS Claim 2; Page 33; 52pp; English.

CC The present sequence is human Bcl-w, a pro-survival member of the

CC Bcl-2 family which is widely expressed and which is essential for

CC spermatogenesis. The invention relates generally to a method of

CC treatment and to an animal model for the identification of

CC molecules and genetic sequences useful for inducing or reducing

CC fertility of male animals. Methods are provided for the treatment

CC of infertility, or for reducing fertility, by modulating

CC spermatogenesis. An animal model carries a mutation is at least

CC one allele of the human or murine bcl-w gene (see X25132-35) or in

CC a gene associated with bcl-w. Such animals have disorganised

CC seminiferous tubules and are substantially infertile, but possess no

CC other major abnormalities as determined by histological examination.

CC They can be used to screen for therapeutic molecules including

CC genetic sequences capable of inducing, enhancing or otherwise

CC facilitating spermatogenesis in animals, or which can induce

CC infertility.

CC Sequence 193 AA;

QY Query Match 99.0%; Score 1383; DB 1; Length 193;

Best Local Similarity 99.0%; Pred. No. 4.66e-122;

Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MATPASAPDTRALVADFGYKLRQGYVCGAGPGEGPAADPLHQAMRAAGDEFFETFRRT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 1 MATPASAPDTRALVADFGYKLRQGYVCGAGPGEGPAADPLHQAMRAAGDEFFETFRRT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 61 FSDLAQLHVTGSAQQRFTQVSDLELFGQGNWGRVAVFFLFGAALCAESVKNEMEPLVG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 FSDLAQLHVTGSAQQRFTQVSDLELFGQGNWGRVAVFFLFGAALCAESVKNEMEPLVG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 121 QVQEMWVAYLETRLDVWIIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 QVQEMWVAYLETRLDVWIIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTGAVAL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 181 GALVTGGAFFASK 193

QY 181 GALVTGGAFFASK 193

RESULT 4

ID Y05531 standard; Protein; 193 AA.

AC Y05531;

DT 05-JUL-1999 (first entry)

DE Mouse Bcl-w protein essential for spermatogenesis.

KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;

KW animal model.

OS Mus sp.

PN W09913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; AU0764.

PR 16-SEP-1997; AU-009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Adams J, Cory S, Gibson L, Koentgen F, Print C;

DR WPI: 99-243890/20.

DR N-PSDB; X25133.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

PT protein associated with Bcl-w

PS Claim 2; Page 35; 52pp; English.

CC The present sequence is mouse Bcl-w, a pro-survival member of the

CC Bcl-2 family which is widely expressed and which is essential for

CC spermatogenesis. The invention relates generally to a method of

CC treatment and to an animal model for the identification of

MPSRCH_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Jun 23 14:13:31 2000; MasPar time 7.29 Seconds
Tabular output not generated.
626.869 Million cell updates/sec

(TM)

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MPSRCH_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Jun 23 14:13:31 2000; MasPar time 7.29 Seconds
Tabular output not generated.
626.869 Million cell updates/sec

Title: >US-09-155-327B-7
Description: (1-193) from US09155327B.pep
Perfect Score: 1397
Sequence: 1 MATPASAPDTRALVADVGVY.....LTCVALGALVTGGAFFASK 193
Scoring table: PAM 150
Gap 11
Searched: 188963 seqs, 23686106 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq36
1:geneseqp
Statistics: Mean 32.637; Variance 140.214; scale 0.233

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

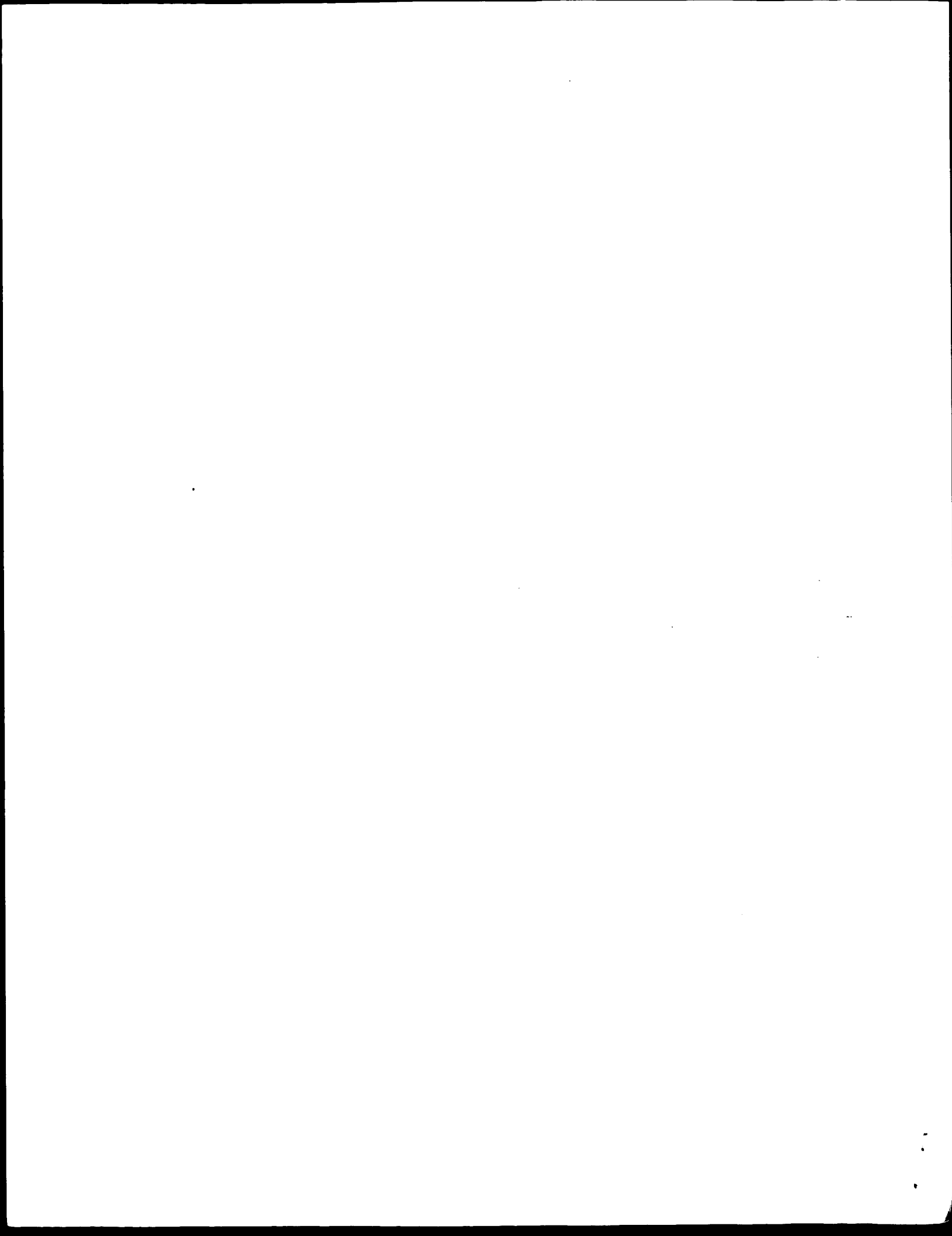
SUMMARIES				Pred. No.	
Result No.	Score	Query Match	Description	ID	
1	1397	100.0	Human Bcl-w protein es	1 Y05532	1.91e-123
2	1397	100.0	Human bcl-w protein.	1 W36047	1.91e-123
3	1383	99.0	Human Bcl-w protein es	1 Y05530	4.66e-122
4	1380	98.8	Mouse Bcl-w protein es	1 Y05531	9.23e-122
5	1379	98.7	Human bcl-y protein.	1 W61392	1.16e-121
6	1379	98.7	The human bcl-y protei	1 W97392	1.16e-121
7	1378	98.6	The rat bcl-y protein.	1 W97391	1.46e-121
8	1378	98.6	Rat bcl-y protein.	1 W61391	1.46e-121
9	1368	97.9	Mammalian bcl-y protei	1 W97394	1.42e-120
10	1367	97.9	Protein sequence of th	1 Y07393	1.79e-120
11	1331	95.3	Mouse Bcl-w protein de	1 Y05533	6.54e-117
12	1202	86.0	Mouse bcl-w sequence.	1 W36048	3.67e-104
13	1049	75.1	Amino acid sequence of	1 W59884	4.39e-89
14	616	44.1	Human thymus BCL-XL.	1 R8887	7.90e-47
15	616	44.1	Bcl-XL protein.	1 W05821	7.90e-47
16	616	44.1	Human anti-apoptotic B	1 W31530	7.90e-47
17	615	44.0	"Deprenyl" (RTM)-induc	1 W19396	9.87e-47
18	586	41.9	Human Bcl-2 protein.	1 W87810	6.14e-44
19	575	41.2	A human Bcl-2-alpha pr	1 W71404	7.02e-43
20	575	41.2	Human bcl-2 alpha prot	1 R71404	7.02e-43
21	575	41.2	Human Bcl-2 protein.	1 R70331	7.02e-43
22	575	41.2	Bcl-2 oncogene product	1 R42312	7.02e-43
23	575	41.2	Human bcl-2.	1 W40217	7.02e-43

24 575 41.2 239 1 P80987 Sequence of bcl-2-alpha 7.02e-43
25 575 41.2 239 1 R47344 Human oncogene bcl-2 p 7.02e-43
26 572 40.9 232 1 W01019 Apoptosis-blocking pro 1.36e-42
27 572 40.9 232 1 W94346 Human Bcl-2 mutant pro 1.36e-42
28 572 40.9 236 1 W87811 A murine Bcl-2 protein 1.36e-42
29 572 40.9 239 1 W94345 Human Bcl-2 wild-type 1.36e-42
30 572 40.9 239 1 W01018 Apoptosis-blocking pro 1.36e-42
31 565 40.4 232 1 W01020 Apoptosis-blocking pro 6.42e-42
32 565 40.4 232 1 W94347 Human Bcl-2 mutant pro 6.42e-42
33 561 40.2 239 1 W02383 Human BCL2. 1.55e-41
34 537 38.4 190 1 R68884 Chicken lymphoid BCL-X 3.12e-39
35 535 38.3 235 1 W48312 Mouse Bcl-x gamma. 4.84e-39
36 499 35.7 205 1 R68886 Human thymus BCL-2. 1.34e-35
37 499 35.7 205 1 W31529 Human anti-apoptotic B 1.34e-35
38 499 35.7 205 1 W71405 Human Bcl-2-beta prote 1.34e-35
39 499 35.7 205 1 R70332 Human bcl-2 beta prote 1.34e-35
40 499 35.7 205 1 W96319 Human bcl-2 protein. 1.34e-35
41 499 35.7 205 1 W96319 bcl-2 polypeptide. 1.34e-35
42 467 33.4 205 1 R80988 Sequence of bcl-2-beta 1.49e-32
43 448 32.1 229 1 W94348 Human Bcl-2 mutant pro 9.46e-31
44 448 32.1 229 1 W01021 Apoptosis-blocking pro 9.46e-31
45 333 23.8 63 1 R68885 Human thymus BCL-X1. 5.77e-20

ALIGNMENTS

RESULT 1
ID Y05532 standard; Protein; 193 AA.
AC Y05532;
DT 05-JUL-1999 (first entry)
DE Human Bcl-w protein essential for spermatogenesis.
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
OS Homo sapiens.
PN W0913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; AU0764.
PR 16-SEP-1997; AU-009228.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR N-PSDB; X25134.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
PS Disclosure; Page 37; 52pp; English.
CC The present sequence is described of a derivative of human Bcl-w
CC (see also Y05530), a pro-survival member of the Bcl-2 family that
CC is widely expressed and which is essential for spermatogenesis.
CC The invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for
CC reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine
CC bcl-w gene (see X25132-35) or in a gene associated with bcl-w.
CC Such animals have disorganised seminiferous tubules and are
CC substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to
CC screen for therapeutic molecules including genetic sequences
CC capable of inducing, enhancing or otherwise facilitating
CC spermatogenesis in animals, or which can induce infertility.
SQ Sequence 193 AA;

Query Match 100.0%; Score 1397; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.91e-123;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MATPASAPDTRALVADVGVYKLRQKGYVCGAGPGGPAADPLHQANRAAGDEFETFRRT 60
QY 1 MATPASAPDTRALVADVGVYKLRQKGYVCGAGPGGPAADPLHQANRAAGDEFETFRRT 60
DB 61 FSDLAQLHVTGSAQRFTQVSDLELFCQGNWGRULVAFFLFGAALCAESVKNEMPLVG 120
|||||



Matches	370;	Conservative	0;	Mismatches	188;	Indels	9;	Gaps	1
QY	16	tcggccccagacacacgggctctgtggtggcagacctttaggtttaaagctgagcgagaag	75						
Db	132	TCGTGACCTAGGATCCCGGCTTTGGTAGAGGATTTGGTAGGTACAAGTTATGCCAGGCT	191						
QY	76	ggttatgtctgtgagctggtgccccggggagggccccagctgacccccctgcacacaagcc	135						
Db	192	AGTCTGTTCCCGAGCCT-----TCAGGAGCAGCATCTGTGCTTTCATTCGGCT	242						
QY	136	atcgaggcagctgagatagattcgagaccgcctccggcgccacctctctctgctatcgcg	195						
Db	243	ATCGGTGCTGACGGGATGAATTTGAGGAGCGAATTCAGACAAGCATTTCAGTGAGATCTCC	302						
QY	196	gtcagctgcatgtgacccagctcagccagcaaccccttcacccaggtctccgacgaa	255						
Db	303	ACACAGATCCATGTGACCCCGGCACAGCATATGCACGCTTTGCACAGAAGTAGCAGGTAGC	362						
QY	256	cttttcaaggggccccaaactggggcgccctgttagccttcttctcttcttcttcttctt	315						
Db	363	CTATTCAAAGTGGGTGAATTTGGGTCGCATAGTTGCATTTTGTGTTTGGTCCCGCG	422						
QY	316	ctgtgtctgagagtgtcaacaaggagatggaaccactggtgggacaagtgcagagtgg	375						
Db	423	CTGTGTGCTGAGAGTGTCAACAAGGAGATGTCCCTCTCTCTGCCACGGATCCAGACTGG	482						
QY	376	atggtggcctacctggagacgcggctggtcgactggatgccacagcagtggggctgggagc	435						
Db	483	ATGCTGACATATCTGAGACAAACCTGAGAGACTGGATTCAGAGCAATGGTGGTGAAT	542						
QY	436	gagttcacagctctatacaggggagcgccctggaggcgcgctctctcgggagggg	495						
Db	543	GGGTTTCTAACTCTATATGGGATGGTGCATAGAGAAGACGAGGAGCAACGTCAGGGG	602						
QY	496	aactgggcatcagtgagacagctgctgacggggggcggtggcactggggcgccctgtaact	555						
Db	603	AAATGGGCACTCATGAAGACTGCTTAACTGGAGCTGTGGCTCTGGGTGCTTTGATGACA	662						
QY	556	gtaggggctttttgctagcaagtga	582						
Db	663	GTAGGGGCTTTGTTGCCAGCAAGTGA	689						
RESULT	10								
LOCUS	RNU10579	764 bp	DNA	ROD				26-JUN-1994	
DEFINITION	Rattus norvegicus Bcl-x (bcl-x) gene, complete cds.								
ACCESSION	U10579								
VERSION	U10579.1	GI:505698							
KEYWORDS	Norway rat.								
SOURCE	Rattus norvegicus								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.								
REFERENCE	1 (bases 1 to 764)								
AUTHORS	Wesselingh,S.L., David,G.L., Choi,S., Veliuona,M. and Hardwick,J.M.								
TITLE	Cloning and expression of rat bcl-x in cultured neurons								
JOURNAL	Unpublished								
REFERENCE	2 (bases 1 to 764)								
AUTHORS	Hardwick,J.M.								
TITLE	Direct Submission								
JOURNAL	Submitted (13-JUN-1994) J. Marie Hardwick, Neurology, Johns Hopkins School of Medicine, 600 North Wolfe St., Baltimore, MD 21287-7681, USA								
FEATURES	Location/Qualifiers								
source	1. .764								
gene	/organism="Rattus norvegicus" /db_xref="taxon:10116" /tissue_type="brain"								
CDS	39. .740								
	/gene="bcl-x"								
	39. .740								
	/gene="bcl-x"								
BASE COUNT	203 a	146 c	224 g	176 t					
ORIGIN									
Query Match									
Best Local Similarity	40.9%;	Score 238.2;	DB 4;	Length 749;					
	65.3%;	Pred. No. 9.3e-44;							

QY	121	ccgctgcaccaagccatcgccgagctgagatagttcagagaccgcttccgcgcacc	180	/note="matching EMBL:AA167748; Identified using the e-PCR software (G. Schuler)"
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Db	299	CGCGTGCACCAAGCCATCGCGCTCTCTGAGACGAGTTTGAGACCCGTTTCCGCCGCACC	358	/standard_name="H79035"
QY	181	ttctctgatctgcggctcagctgcatgaccccccagctcagcccccagcaacgcttcacc	240	/note="matching EMBL:H79035; Identified using the e-PCR software (G. Schuler)"
Db	359	TTCTCTGACCTGGCGCTCAGCTACACGTGACCCCGAGCTCAGCCAGCAACGCTTCACC	418	93575. .93803
QY	241	caagttccgacgaacttttcaagggggccccaactggcccttgtagcctcttt	300	/standard_name="AA007328"
Db	419	CAGGTTCCGACGAACCTTTTCAAGGGGGCCCTAACTGGGCCGCTCTGTGGCAATCTTT	478	/note="matching EMBL:AA007328; Identified using the e-PCR software (G. Schuler)"
QY	301	ctctttgggctgactgtgtgtagagagtgcacaaggagatggaaccactggtggga	360	107753. .107946
Db	479	GNCTTTGGGCTGCCCTGTGCTCAGAGAGTGTCAACAAGAAATGGAGCCTTTGTGGGA	538	/standard_name="R94929"
QY	361	caagtgcagagatgagtggtgcctacctgagagacgcgctggtgcactgacccacgc	420	/note="matching EMBL:R94929; Identified using the e-PCR software (G. Schuler)"
Db	539	CAAGTGCAGGATTTGATGTTGCGCTACCTCGGAGACACGCTCTGGCTAGTGCATCACACG	598	107991. .108176
QY	421	agtgggggctggcgagttcacagctctctacggggcgccgctggagggcgcg	480	/standard_name="D11677"
Db	599	AGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGACGGGGCCCTGGAGGACACCG	658	/note="matching EMBL:D11677; Identified using the e-PCR software (G. Schuler)"
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Db	659	CGTCTCGGGAGGGGAACCTGGGCATCAGTGAAGACAGTCTGCTGACGGGGCCGTGGCACTG	718	/standard_name="H22648"
QY	541	ggggccctgtaactgtaggcccttttttctgtagcaagtga	582	/note="matching EMBL:H22648; Identified using the e-PCR software (G. Schuler)"
Db	719	GGGGCCCTGTTACTGTAGGGCCCTTTTGTGTAGCAAGTGA	760	128415. .128539
RESULT	8			
CNS00000B				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
STS				
STS				

On Oct 28, 1999 this sequence version replaced gi:4972127.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from *E.coli*, yeast, vector, phage, etc. XX.

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80431..80564
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AUTHORS Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and Cory, S.

TITLE Direct Submission

JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia

FEATURES

source

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RLREGNWSVTVLTGVALGALVTVGAFFASK"

BASE COUNT 107 a 158 c 200 g 117 t

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Best Local Similarity 93.6%; Pred. No. 2.4e-107;
Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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Qy 541 ggggcccctgtaactgtaggggctttttgtctagcaagtga 582
Db 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582

RESULT 7

AF030769

LOCUS

DEFINITION

AF030769

ACCESSION

AF030769.1

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..3476

/organism="Mus musculus"

/strain="C57BL/10J"

/db_xref="taxon:10090"

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1..82

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171..610

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179..760

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611..3476

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3356..3364

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3428..3441

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BASE COUNT 796 a 814 c 991 g 875 t

ORIGIN

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Best Local Similarity 93.6%; Pred. No. 2e-107;

Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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Db 239 AAGCTGAGGAGAGAGGTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGCCGAC 298

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BASE COUNT 804 a 817 c 1030 g 891 t
ORIGIN

Query Match 98.6%; Score 575; DB 9; Length 3542;
Best Local Similarity 99.1%; Pred. No. 4.2e-119;
Matches 578; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db 177 ATGGGACCCAGCCTCGGCCCCAGACACACAGCGCTCTGGTGGCAGACTTTGTAGGTTAT 236
QY 61 aagctgagcagaagaaggttatctgtgagctgccccggggagggccccagcagctgac 120
Db 237 AAGCTGAGCAGAAAGGTTATGCTGTGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 296
QY 121 ccgctgcaccaaagccatcgccgagctgagatgagttcgagaccgccttccggcgaccc 180
Db 297 CGCTGACCAACCACTGCGGCGCAGCTGGAGATGAGTTTCGAGACCCCGCTTCGGCGCACCC 356
QY 181 ttctctgatctggcgctcagctgacatgacccagctcagccccagcagcagcttcacc 240
Db 357 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAGCTCAGCCCAACAACGGCTTCACC 416
QY 241 caggtctccagcagaacttttcaagggggccccaaactggcgcccttgtagccttcttt 300
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QY 301 ctcttgggctgactgtgtcagagtgatcaacagagagatggaacacactggtggga 360
Db 477 GTCCTTGGGCTGCACTGTGTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 536
QY 361 caagtgcaggagtgatggtgacctacctggagacgcggtggtgactggtatccacagc 420
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QY 481 cgtctgcggaggggaactgggcatcagtgagagcagtgctgacggggcgctggtgacatg 540
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QY 541 ggggccccgtgaactgtaggggccctttttgtctagcagaagttaa 583
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RESULT 3
AR020780
LOCUS AR020780 579 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5789201.
ACCESSION AR020780
VERSION AR020780.1 GI:3975395
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 579)
AUTHORS Guastella,J.
TITLE Genes coding for bcl-y a bcl-2 homologue
JOURNAL Patent: US 5789201-A 2 04-AUG-1998;
FEATURES Location/Qualifiers
source 1. 579
BASE COUNT 106 a 154 c 208 g 111 t
ORIGIN

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QY 61 aagctgagcagaagaaggttatctgtgagctgccccggggagggccccagcagctgac 120
Db 61 AAGCTGAGGAGCAAGAGGTTATGCTGTGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120
QY 121 ccgctgcaccaaagccatcgccgagctgagatgagttcgagaccgccttccggcgaccc 180
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QY 181 ttctctgatctggcgctcagctgacatgacccagctcagccccagcagaacgcttcacc 240
Db 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAGCTCAGCCCAACAACGCTTCACC 240
QY 241 caggtctccagcagaacttttcaagggggccccaaactggggcccttgtagccttcttt 300
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QY 421 agtggggctggcgaggttcaactctatatacggggacggggccccctggagagcgcg 480
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QY 541 ggggccccgtgaactgtaggggccctttttgtctagcagaag 579
Db 541 GGGGCCCTGTAACGTAGGGGCCCTTTTGTCTAGCAAG 579

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LOCUS Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds. 15-OCT-1998
DEFINITION Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION AF096291
VERSION AF096291.1 GI:3747129
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 582)
AUTHORS Hamner,S., Skoglosa,Y. and Lindholm,D.
TITLE Differential expression of Bcl-w and Bcl-x mRNA in the developing
and adult nervous system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 582)
AUTHORS Hamner,S., Skoglosa,Y. and Lindholm,D.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
University, Box 587, BMC, Uppsala 751 23, Sweden
FEATURES Location/Qualifiers
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ACCESSION U59747
VERSION    U59747.1 GI:1572492
KEYWORDS   human.
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 582)
AUTHORS    Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
            Cory, S.
            Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
            Eliza Hall Institute of Medical Research, PO Royal Melbourne
            Hospital, Parkville, Victoria 3050, Australia
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Best Local Similarity 99.5%; Pred. NO. 1.6e-119;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 61 aagctgagggcagaggttatgtctgtgagctgccccgggagggccagcagctgac 120
Db 61 AAGCTGAGGCAGAGAAGGTTATGTCTGTGAGCTGGCCCCGGGGAGGCCACAGCTGAC 120
QY 121 ccgctgcacaaagccatcgggcagctggagatgattcgagaccgcttcggcgacc 180
Db 121 CCGCTGCACAAAGCCATCGGGCAGCTGGAGATGAGTTTCGAGACCGCTTCGGGGCACC 180
QY 181 ttctctgatctggcgctcagctgcatgtgacccagctcagccagcagcttcacc 240
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QY 301 ctcttggggctgcactgtgtgtgagatgtcaacaaggagatggaaccactggtgga 360

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Db 301 GTCTTTGGGCTGCTGTGTGTGAGAGTGTCAACAAGGAGATGGAACCACTGTTGGGA 360
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Db 361 CAAAGTCAGAGTGGATGGTGGCTTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420
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QY 481 cgtctcgaggaggggaactgggcatcagtgagagcagtgctgacggggggccctggcactg 540
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QY 541 ggggcccctgtaactgtaggcgcttttttttcttagcaagtga 582
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RESULT 2
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LOCUS      D87461      3542 bp      mRNA      PRI      10-JUL-1997
DEFINITION Human mRNA for KIAA0271 gene, complete cds.
ACCESSION D87461
VERSION    D87461.1 GI:1944417
KEYWORDS   KIAA0271.
SOURCE     Homo sapiens male brain myeloblast cell_line:KG-1 CDNA to mRNA,
            clone_lib:psport 1 clone:HA6752.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 3542)
AUTHORS    Nomura, N.
            Direct Submission
            Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobuo
            Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3
            Yana, Kisarazu, Chiba 292, Japan (E-mail:cdmainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931)
            2 (sites)
            Nagase, T., Seki, N., Ishikawa, K. and Nomura, N.
            Prediction of the coding sequences of unidentified human genes. VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from human cell line KG-1 and brain
            Unpublished (1996)
            3 (sites)
            Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayashi, Y.,
            Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and Nomura, N.
            Prediction of the coding sequences of unidentified human genes. VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from cell line KG-1 and brain
            DNA Res. 3 (5), 321-329 (1996)
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2000, 20:45:19 ; Search time 888.39 Seconds
(without alignments)
-638.388 Million cell updates/sec

Title: US-09-155-327B-6

Perfect score: 583

Sequence: 1 atggcagcccccagctcggc.....ctttttgctagcaagtga 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_om.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl1.*
- 8: gb_pl2.*
- 9: gb_pr1.*
- 10: gb_pr2.*
- 11: gb_pr3.*
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- 13: gb_sts.*
- 14: gb_sy.*
- 15: gb_un.*
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- 51: gb_pr5.*
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- 53: gb_htg9.*
- 54: gb_htg10.*
- 55: gb_htg11.*
- 56: gb_htg12.*
- 57: gb_htg13.*
- 58: gb_htg14.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	577.2	99.0	582	10	HSU59747
2	575	98.6	3542	9	D87461 Human bcl-w
3	567.8	97.4	579	5	AR020780 Sequence
4	527.6	90.5	582	12	AF096291
5	523	89.7	579	5	AR020779 Sequence
6	522.8	89.7	582	12	MMU59746
7	522.8	89.7	3476	12	AF030769 Mus muscu
8	423.4	72.6	196287	10	CNS00000B
9	238.2	40.9	749	4	XLR1
10	143	24.5	764	12	RNU10579
11	143	24.5	1742	12	RNU72350
12	143	24.5	2232	12	RNCBLXLS
13	138.2	23.7	726	12	RNU34963
14	138.2	23.7	726	12	S76513
15	135.6	23.3	720	3	AF216205
16	135.6	23.3	752	3	SSJ001203
17	132.8	22.8	699	12	MMBCLXL
18	132.8	22.8	702	12	MMU10101
19	132.8	22.8	979	12	MUSBCLX
20	132.8	22.8	1466	12	MMU51278
21	132.8	22.8	5771	14	AF060226
22	131	22.5	926	5	AR054021
23	131	22.5	926	5	I52011
24	131	22.5	926	9	HSBCLXL
25	129.8	22.3	1748	12	RNU72349
26	128.6	22.1	708	12	RNU34964
27	128.2	22.0	687	3	BTU92434
28	127	21.8	1179	12	RATBCL2A
29	127	21.8	1184	4	GGU26645
30	123.4	21.2	717	5	AR052622
31	123.4	21.2	765	5	A76121
32	123.4	21.2	5086	5	AR052621
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34	123.4	21.2	5086	5	HUMBCL2A
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38	123.2	21.1	151029	33	HSJ857M17
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ALIGNMENTS

Qy 451 tacgg 455
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Db 2062 TACGG 2066

Search completed: July 4, 2000, 01:24:21
Job time: 14809 sec

Wed Jul 5 11:21:22 2000

QY	421	agtgggggctggcgagttcacagctctatcacggggacggggcccttgaggagggcgccg	480
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QY	481	cgtctcggaggggaaactgggcagtcagtgagagcagtgctgacgggggcgtgggcacitg	540
Db	481	CgtCtGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTCTGACGGGGGCTGTGGCACTG	540
QY	541	ggggccctgtaactgtaggggccttttttctgtagcaag	579
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RESULT 5			
US-08-081-448-5			
; Sequence 5, Application US/08081448			
; Patent No. 5646008			
; GENERAL INFORMATION:			
; APPLICANT: Thompson, Craig B.			
; APPLICANT: Boise, Lawrence H.			
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:			
; TITLE OF INVENTION: Compositions and Methods			
; NUMBER OF SEQUENCES: 8			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Arnold, White & Durkee			
; STREET: 321 No. 5646008th Clark Street, Suite 800			
; CITY: Chicago			
; STATE: IL			
; COUNTRY: USA			
; ZIP: 60610			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/081,448			
; FILING DATE: 19930622			
; CLASSIFICATION: 424			
; ATTORNEY/AGENT INFORMATION:			
; NAME: NO. 5646008thrup, Thomas E.			
; REGISTRATION NUMBER: 33,268			
; REFERENCE/DOCKET NUMBER: ARCD090			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 312-744-0090			
; TELEFAX: 312-755-4489			
; INFORMATION FOR SEQ ID NO: 5:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 926 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (genomic)			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 135..836			
; US-08-081-448-5			

Db	484	GGACAGCATATCAGAGCTTTGAACACGGTAGTGAATGAACCTCTTCCGGGATGGGTAAACT	543
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Db	544	GGGTGCGATGTGGCTTTTCTCTCGCGGGCACCTGTGCGTGGAAGCGTAGACA	603
Qy	338	agagatggaaccacttggtgggacaaagtgcagagtcagatggttgccctaccctggagacgc	397
Db	604	AGGAGATGCAAGGTATTGGTGAGTCGGATCCACAGCTTGGATGGGCACCTTACCTGAATGACC	663
Qy	398	ggctggctcgcactgataccacagcagtcagtggggctggggcgaggttccacagctctatacgggg	457
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Qy	458	acggggccctggaggagcgccggtctctcgggaggggaaactggggcatcagtgagagacag	517
Db	724	ACAATGCAGCAGCGAGAGCGGAAGGCGCAGGAACGCTTCAACCGTGCTTCTGACGG	783
Qy	518	tgctgacggggggccg	532
Db	784	GCATGACTGTGGCCG	798
RESULT 6			
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; Sequence 6, Application US/08470670A			
; Patent No. 5834309			
; Patent No. 5834309 5710045			
GENERAL INFORMATION:			
; APPLICANT: Thompson, Craig B. B.			
; APPLICANT: Boise, Lawrence H.			
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS			
; NUMBER OF SEQUENCES: 18			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Arnold, White & Durkee			
; STREET: P. O. Box 4433			
; CITY: Houston			
; STATE: Texas			
; COUNTRY: United States of America			
; ZIP: 77210			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA: US/08/470,670A			
; FILING DATE:			
; CLASSIFICATION: 514			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/081,448			
; FILING DATE: 22-JUN-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Highlander, Steven L.			
; REGISTRATION NUMBER: 37,642			
; REFERENCE/DOCKET NUMBER: ARCD:090--1			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (512) 418-3000			
; TELEFAX: (512) 474-7577			
; INFORMATION FOR SEQ ID NO: 6:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 926 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; FEATURE:			
; NAME/KEY: CDS			
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US-08-470-670A-6			

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-08-798-897-1

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Query Match	89.7%	Score 523;	DB 2;	Length 579;	
Best Local Similarity	94.0%;	Pred. No. 1e-124;			
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QY	61	aagctgaggcgaaagggttatgtctgtggagctggccccggggagggccacagcagctgac	120		
Db	61	AAGCTGAGACAGAAGGTTATGTCGTGGAGCTGSCCCTGSGGAAGGCCAGCAGCCGAC	120		
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QY	181	ttctctgatctggcgctcgagctgcattgaccccaggctcagccagcaacgcttcacc	240		
Db	181	TTCTCTGACCTGGCGCTCAGCTACAGTGCACCCAGGCTCAGCCCAAGCAACGCTTCACC	240		
QY	241	caggtctccgacgaactttttcaagggggggcccaactggggcgcccttgtagcctctttt	300		
Db	241	CAGGTTTCGACGAACTTTTCCAAAGGGGGCCCAACTGGGGCCGCTCTGTGGCATTCCTT	300		
QY	301	ctctttggggctgcactgtctcgagatgtcaacaagagagatggaaccaactggtgga	360		
Db	301	GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCACAAAGAAATGGAGCCATTGGTGGGA	360		
QY	361	caagtgcaggatggatggctgacctggagacggcgctggctcgactggatccacagc	420		
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QY	421	agtgggggctggcgagattcaacagctctatacggggacggggccctcggaggagcgcg	480		
Db	421	AGTGGGGGCTGGCGAGATTCAAGCTCTATACGGGGACGGGGCCCTTGGAGGAGCACGG	480		
QY	481	cgctcggggaggggaactgggcatacgtgaggacagtgctgacggggccgtggcacctg	540		
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QY	541	ggggcccttggtaactbtaggggccttttttctctagcaag	579		
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RESULT 4
US-08-978-523-1
; Sequence 1, Application US/08978523
; Patent No. 5883229

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1  / GENERAL INFORMATION:
2  / APPLICANT: Guastella, John
3  / TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
4  / TITLE OF INVENTION: Homologue
5  / NUMBER OF SEQUENCES: 53
6  / CORRESPONDENCE ADDRESS:
7  / ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
8  / STREET: 1100 New York Avenue, N.W., Suite 600
9  / CITY: Washington
10 / STATE: DC
11 / COUNTRY: USA
12 / ZIP: 20005
13 / COMPUTER READABLE FORM:
14 / MEDIUM TYPE: Floppy disk
15 / COMPUTER: IBM PC compatible
16 / OPERATING SYSTEM: PC-DOS/MS-DOS
17 / SOFTWARE: PatentIn Release #1.0, Version #1.30
18 / CURRENT APPLICATION DATA:
19 / APPLICATION NUMBER: US/08/978,523
20 / FILING DATE: herewith
21 / CLASSIFICATION: 424
22 / PRIOR APPLICATION DATA:
23 / APPLICATION NUMBER: US 08/798,897
24 / FILING DATE: February 11, 1997
25 / CLASSIFICATION: 424
26 / ATTORNEY/AGENT INFORMATION:
27 / NAME: Esmond, Robert W.
28 / REGISTRATION NUMBER: 32,893
29 / REFERENCE/DOCKET NUMBER: 1483.0140002
30 / TELECOMMUNICATION INFORMATION:
31 / TELEPHONE: 202-371-2600
32 / TELEFAX: 202-371-2540
33 / INFORMATION FOR SEQ ID NO: 1:
34 / SEQUENCE CHARACTERISTICS:
35 / LENGTH: 579 base pairs
36 / TYPE: nucleic acid
37 / STRANDEDNESS: both
38 / TOPOLOGY: both
39 / MOLECULE TYPE: CDNA
40 / US-08-978-523-1

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Query Match	89.7%	Score 523;	DB 3;	Length 579;
Best Local Similarity	94.0%;	Pred. No. 1e-124;		
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Qy	61	aagctgagggcagaaggttatgtctgtggaagtgcgcccggggagggccacagcagctgac	120	
Db	61	AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGCGCCTGGGGAAGGCCACAGACCGAC	120	
Qy	121	ccgctgaccaaagccatgcgggcagctggagatgagttcagacccgcttcgcggcgacc	180	
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RESULT 13
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LOCUS
DEFINITION
W01420 437 bp mRNA EST 18-APR-1996
IMAGE:298187.5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
BCL-X.; mRNA sequence.
ACCESSION
VERSION
W01420.1 GI:1273428
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 437)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisakis,E., Waterston,K., Williamson,A., Wohldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785898.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 383.
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1. .437
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/dev_stage="19 weeks"
/lab_host="DH108 (ampicillin resistant)"
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strand cDNA was primed with a Not I - oligo(dT) primer
15'-TGTTACCAATCTGAAGTGGGAGCGCGCAATTTTTTTTTTTT-3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
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BASE COUNT 99 a 106 c 140 g 89 t 3 others
ORIGIN

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Best Local Similarity 62.9%; Pred. No. 5.4e-17;
Matches 193; Conservative 0; Mismatches 113; Indels 1; Gaps 1;
Qy 128 accaagccatcgggcagctggagatgagtcgagaccgcttcgcgagcactctctg 187

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Db 16 ACCAAGCGCTGAGGAGGAGCGAGCTTGAACCTGGGTACCGGGCGGCAATCACTG 75
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AT401297/c
AT401297 471 bp mRNA EST 30-MAR-1999
IMAGE:29206.x1 NCI-CGAP-CLL1 Homo sapiens cDNA clone IMAGE:2116234 3'
similar to gb:MI3995 PROTEIN BCL-2-BETA (HUMAN); contains TAR1.t2
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ACCESSION
VERSION
AT401297.1 GI:4244384
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 471)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Apr 7, 1998 this sequence version replaced gi:3035272.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2629 Std Error: 0.00
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High quality sequence stop: 445.
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/clone_lib="NCI-CGAP-CLL1"
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/lab_host="DH108"
/notes="Vector: pRT3D-Pac (Pharmacia) with a modified
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was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCAATTTTTTTTTTTT-3'];
double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT3 vector.

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FEATURES

source

(Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG_LJB=UI-R-YO
TAG_TISSUE=Eye
TAG_SEQ=CATTG*
BASE COUNT 88 a 128 c 92 g 96 t
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Best Local Similarity 61.4%; Pred. No. 1.1e-19;
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Db 323 AACTCGGTACCGGAGAGCATTCAGTGTCTTAACATCCAGCTTCAATATAACCCAGGGA 264
Qy 221 cagccagcaacgttcacccaggtctccgacgaacttttcaagggggcccaactggg 280
Db 263 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACACTCTTTCGGGATGGGGTAACTGGG 204
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Db 203 GTCCGATGTGGCTCTTCTCTCTTGGCGGGGACATGTGCGTGGAAAGCGTAGACAAGG 144
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Db 83 TAGAGCCTTGGATCCAGGAGAACGGCGGC 55

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SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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DKF2P547K2090_r1 547 (synonym: hfb1) Homo sapiens cDNA clone
DKF2P547K2090 5', mRNA sequence.
AL134785
AL134785.1 GI:6602972
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 584)
Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).
EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).
Wiemann, S.)
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5866255.
Contact: Poustka A.J.
Department Leirach
Max-Planck-Institute for Molecular Genetics
Ihnstrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source

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1. 584
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/db_xref="taxon:9606"
/clone="DKF2P547K2090"
/clone_lib="547 (synonym: hfb1)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/note="Vector: pAMP1; Site_1: 116 t
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ORIGIN

Query Match 20.5%; Score 119.4; DB 79; Length 584;
Best Local Similarity 60.2%; Pred. No. 3.7e-18;
Matches 192; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
Qy 98 ccggggagggccagcagctgacccgctgcacacagccatgcggcagctggagatgag 157
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Qy 158 tcgagaccgcttcggcgacattctctgctgctggcgctcagctgctgacgtgacccag 217
Db 323 TTGAACCTGCGGTACCGCGCGGCGATTCAGTGACCTGACATCCAGCTCCACATCACCAG 382
Qy 218 gctcagccagcaacgcttcacccaggtctccgacgaacttttcaagggggcccaact 277
Db 383 GGACAGCATATCANAGCTTTGAACAGGTAGTGAATGAACACTCTTCGGGATGGGTAAACT 442
Qy 278 gggggcgccttgaccccttctcttcttctggggctgacgtgctgctgagatgcaaca 337
Db 443 GGGGTGCGATTGTGGCTTTTCTCTCTGGCGGGCGACTGTGCTGGAAGCGGTAGACA 502
Qy 338 aggagatggaaccactggtgggacaagtcagagtgatggtgcttaccctggagacgc 397
Db 503 AGGAGATGCANGTATTGGTGTAGTCCNGATCGCATTGGATGCCACTTACCTTGAATGACC 562
Qy 398 ggtggtgactggtatcca 416
Db 563 ACCTANANNCTTGGATCCA 581

RESULT 11
AL124015/c
LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
AL124015 454 bp mRNA EST 22-OCT-1999
UI-M-BH2.1-apn-b-04-0-UI.s1 NIH_BMAP_M_S3.1 Mus musculus cDNA clone
UI-M-BH2.1-apn-b-04-0-UI 3', mRNA sequence.
AL124015
AL124015.1 GI:6099545
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 454)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
On Jul 7, 1999 this sequence version replaced gi:5866278.
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH

```

Query Match      25.5%; Score 148.8; DB 109; Length 549;
Best Local Similarity 98.7%; Pred. No. 5.5e-25;
Matches 150; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 432 ggcggagttcacagctctatcaggggagcggccctgagagcggcgctctgcggga 491
|||||
DB 261 GCGGAGTTCACAGCTCTATACGGGACGGAGCCCTGGAGGAGCGCGGCTCTGCGGGA 320
|||||
QY 492 ggggaactgggcatcagtgagacagtgctgacggggccgtggcaactggggccctggt 551
|||||
DB 321 GGGGAAC TGGGCATCAGTCAGTGAGCACAGTCTGACGGGGCCGTGGCACTGGGGCCCTGGT 380
|||||
QY 552 aactgtagggccttttttgcctagcaagtga 583
|||||
DB 381 AACTGTAGGGCCCTTTTGTGTAGCAAGTGAA 412
|||||

RESULT 8
LOCUS      AQ401160      455 bp      DNA      GSS      13-MAR-1999
DEFINITION HS_5062_A2_G02_SP6E RPCI-11 Human Male BAC Library Homo sapiens
             genomic clone Plate-638 Col=4 Row=M, genomic survey sequence.
ACCESSION  AQ401160
VERSION     AQ401160.1 GI:4412503
KEYWORDS    GSS
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 455)
AUTHORS     Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
             Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
             Hood,L.
TITLE       Sequence-tagged connectors: A sequence approach to mapping and
             scanning the human genome
JOURNAL     Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE     99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
             High Throughput Sequencing Center
             University of Washington
             401 Queen Anne Avenue North, Seattle, WA 98109, USA
             Tel: (206) 616-3618
             Fax: (206) 616-3887
             Email: jwallace@u.washington.edu
             Clones are derived from the human BAC library RPCI-11. For BAC
             library availability, please contact Pieter de Jong
             (pieter@dejong.med.buffalo.edu). Clones may be purchased from
             BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
             or from Resear h Genetics (info@resgen.com). BAC end Web Server:
             http://www.htsc.washington.edu
             Plate: 638 row: M column: 4
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 455.
FEATURES
Source
1. 455
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-638 Col=4 Row=M"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT 80 a 111 c 142 g 117 t 5 others
ORIGIN

Query Match      23.3%; Score 135.6; DB 106; Length 455;
Best Local Similarity 92.8%; Pred. No. 5.9e-22;
Matches 141; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 432 ggcggagttcacagctctatcaggggagcggccctgagagcggcgctctgcggga 491
|||||
DB 224 GCGGAGTTCACAGCTCTATACAGTCACAGCCCTGGAGGATGCGCGCTCTGCGGGA 283
|||||
QY 492 ggggaactgggcatcagtgagacagtgctgacggggccgtggcaactggggccctggt 551
|||||
DB 284 GGGGAAC TGGGCATCAGTCAGTGAGCACAGTCTGACNGTGGCGGTGGCACTTGGGGCCCTTGT 343
|||||
QY 552 aactgtagggccttttttgcctagcaagtga 583
|||||
DB 344 AACTGTAGGGCCCTTTTGTGTAGCAAGTGAA 375
|||||

RESULT 9
LOCUS      AI716839/c 404 bp      mRNA      EST      10-JUN-1999
DEFINITION UI-R-Y0-acg-g-07-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone
             UI-R-Y0-acg-g-07-0-UI 3', mRNA sequence.
ACCESSION  AI716839
VERSION     AI716839.1 GI:5034095
KEYWORDS    EST.
SOURCE      Norway rat.
ORGANISM    Rattus norvegicus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1 (bases 1 to 404)
AUTHORS     Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
             discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
COMMENT     On May 18, 1998 this sequence version replaced gi:3136946.
             Contact: Soares, MB
             Program for Rat Gene Discovery and Mapping
             University of Iowa
             451 Eckstein Medical Research Building Iowa City, IA 52242, USA
             Tel: 319 335 8250
             Fax: 319 335 9565
             Email: msoares@blue.weeg.uiowa.edu
             Oligo-dt track not found, Not I site shown in beginning of sequence
             is likely internal to the message. cDNA Library Preparation: M.B.
             Soares Lab Clone distribution: Clones will be available through
             Research Genetics (www.resgen.com)
             Seq primer: M13 Forward
             POLYA=No.
FEATURES
Source
1. .404
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="UI-R-Y0-acg-g-07-0-UI"
/clone_lib="UI-R-Y0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7m3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dt track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTs had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-Y0
library. This procedure has been previously described
```


QY 61 aagctgagcagaaggttatctgtgagctgccccgggagggccagcagctgac 120
 |||||
 Db 214 AGCTGAGGCAAGAGGGTATGTTGTGGAGCTGGCCCCGGGGAGGCCACGACGTGAC 273
 |||||
 QY 121 ccgtgcaccagccatcgccgagctggagatgagttcgagacccttcctccgagcacc 180
 |||||
 Db 274 CCGCTACACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGCAC 333
 |||||
 QY 181 ttctctgctgagcagctcagctcagctgagccagccagctcagccagcagcttcaacc 240
 |||||
 Db 334 TTCTCCGATCTGGCAGCTCAGCTCATGTGACCCCGGCTCGGCCACGACACGCTTCACC 393
 |||||
 QY 241 caggtctccgacgaacttttcaagggggcccccaactggg 280
 |||||
 Db 394 CAGGTCTCTGATGAACCTTCCAGGGGGCCCCCACTGGG 433
 |||||

RESULT 4
 AW159063
 LOCUS AW159063 416 bp mRNA EST 05-NOV-1999
 DEFINITION za50h02.x1 Xenopus EST library Xenopus laevis cDNA clone za50h02
 5', mRNA sequence.
 ACCESSION AW159063
 VERSION AW159063.1 GI:6271092
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae;
 Xenopus.
 REFERENCE 1 (bases 1 to 416)
 AUTHORS Schutz,K., de la Bastide,M., Huang,E.N., Nascimento,L., Preston,R.,
 Shah,R., Swaby,I., Shekher,M., Spiegel,L., Vil,M.D. and
 McCombie,W.R.
 TITLE Expressed sequence tags from Xenopus
 JOURNAL Unpublished (1999)
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3189433.
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: za50 row: h column: 02
 Seq primer: M3 universal forward primer
 High quality sequence stop: 416.
 Location/Qualifiers
 1..416
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="za50h02"
 /clone_lib="Xenopus EST library"
 /tissue_type="total brain tissue"
 /cell_lines="W22-TGA"
 /dev_stage="tadpole"
 /note="vector: Lambda Zap I; Site 1: XbaI; This library
 was supplied by Holly Cline (Cold Spring Harbor Labs).
 cDNA synthesis with oligo dr Xba I (Xba I cloning site).
 RNA: stage 50-56 tadpoles, total brain tissue, GTC
 extraction method."

FEATURES

source
 1..416
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="za50h02"
 /clone_lib="Xenopus EST library"
 /tissue_type="total brain tissue"
 /cell_lines="W22-TGA"
 /dev_stage="tadpole"
 /note="vector: Lambda Zap I; Site 1: XbaI; This library
 was supplied by Holly Cline (Cold Spring Harbor Labs).
 cDNA synthesis with oligo dr Xba I (Xba I cloning site).
 RNA: stage 50-56 tadpoles, total brain tissue, GTC
 extraction method."

BASE COUNT 108 a 70 c 118 g 120 t
 ORIGIN
 Query Match 27.5%; Score 160.6; DB 71; Length 416;
 Best Local Similarity 72.5%; Pred. NO. 9.2e-28;
 Matches 208; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 296 tttctcttttgggctgactgtgtgctgagagtgtaaacagagagatgaaccactgg 355
 |||||
 Db 5 TTTTCTTTTGGTCCGCACTGTGTGCTGAGAGTGTCAACAGGAGATGTCCTCTCTC 64
 |||||

QY 356 tgggacaagtgcaggagtgatgggtgacctgagacgcggtggtcgactgatcc 415
 |||||
 Db 65 TGCACGGATTCAGACTGGATGGTGACATATCTGGAGACAACCTGAGAGCTGGATTC 124
 |||||
 QY 416 acagcagtggggctggcgaggttcaacagctctatacaggggagcggccctggggaggg 475
 |||||
 Db 125 AGAGCAATGGATGCTGGAATGGATTTCTTAACCTCTATATGGGATGTCCTCAATAGAGAAG 184
 |||||
 QY 476 cgcggtctcgagaggggaaactgagcatcagtagacacagtgctgacgggggcccgtgg 535
 |||||
 Db 185 CCAGGAGGCAACCTGAGGGGAATTTGGGCATCACTGAAGACTGTCTTAACCTGAGCGGTAG 244
 |||||
 QY 536 cactggggccctggttaactgtagggcccttttttctagtagcaagtga 582
 |||||
 Db 245 CTCTGGGTGCTTTGATGACAGTAGGAGCCTGTGTTGCCAGCAAGTGA 291
 |||||

RESULT 5
 AW048567/c
 LOCUS AW048567 431 bp mRNA EST 18-SEP-1999
 DEFINITION UI-M-BH1-alc-e-10-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
 UI-M-BH1-alc-e-10-0-UI 3', mRNA sequence.
 ACCESSION AW048567
 VERSION AW048567.1 GI:5909096
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 431)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT On Feb 18, 1999 this sequence version replaced gi:4297581.
 Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mest@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 normalized corpus striatum library cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
 available by the means that is soon to be determined. When NIH
 determines the means for distribution of the BMAP cDNA clones, this
 record will be updated accordingly when that means is determined.
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..431
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH1-alc-e-10-0-UI"
 /clone_lib="NIH_BMAP_M_S2"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NIH_BMAP_M_S2 library is a subtracted library derived from
 NIH_BMAP_M_S1, which in turn is a subtracted library
 derived from a mixture of normalized libraries from ten
 regions of the mouse brain (cerebellum, brain stems,
 olfactory bulbs, hypothalamus, cortex, amygdala, basal
 ganglia, pineal gland, striatum, hippocampus). The driver

Db	531	AGTGGGGGCT	540
RESULT	2		
AA596919			
LOCUS			
DEFINITION			
AA596919 362 bp mRNA EST 19-SEP-1997 vo21f08.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1050567 5' similar to TR:E123735 E123735 R1 MRNA.; , mRNA sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
The WashU-HHMI Mouse EST Project Unpublished (1996) On Dec 18, 1996 this sequence version replaced gi:1734345. Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:582143 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 334. Location/Qualifiers 1..362 /organism="Mus musculus" /strain="C3H" /db_xref="taxon:10090" /clone="IMAGE:1050567" /clone_lib="Barstead mouse myotubes MPLRB5" /cell_lines="C2C12" /lab_host="DH10B" /note="Vector: pRTD-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTTT 3'] double-stranded cDNA was ligated to Eco RI adaptors [AATCGCATCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins." BASE COUNT 64 a 116 c 107 g 75 t ORIGIN			
Query Match	49.4%;	Score 288;	DB 35; Length 362;
Best Local Similarity	91.1%;	Pred. No. 2.6e-57;	
Matches 306;	Conservative 0;	Mismatches 30;	Indels 0; Gaps 0;
QY	4	gcgaccagcctcgcccccagacacacagggtctctgggtggcagactttgtaggtataag	63
Db	27	GGGACCCCAGCCTCAACCCAGACACACGGGTCTAGTGGGTGACTTTGTAGGTATAAG	86
QY	64	ctgaagcagaaggttatctctgttgagtgcgcccgaggggccccagcagctgacccg	123
Db	87	CTGAGGCAGAAGGGGTATGTCTGTGTGAGCTGCCCTGGGGAGGCCCGCGCGCCG	146
QY	124	ctgcaccaagccatcgggcagctgtagatgagtttcgagaccgcttccggcgacacctc	183
Db	147	CTGCACCAGCCCATGCTGCTGCTGGAGAGGAGTTTGTGAGACCGCTTTCGCCGCACCTTC	206
QY	184	tctgatctggcgctcagctgcatgtgaccccaaggctcagccagcaacgcttccaaccag	243
Db	207	TCTGAATCGGCCCTCAGCTACAGTACAGTGCACCCAGGCTCAGCCAGCACGCTTCACCCAG	266
QY	244	gtctccagacaacttttcaagggggggcccaactggggcgcccttgtagctctttcttc	303
Db	267	GTTTCGACAGAACTTTTCCAAGGGGGCCCTTAAGTGGGGCGCTTGTGTGGCATTCCTTTGTC	326
QY	304	tttggggtgcactgtgctgagagtgtaacaag 339	
Db	327	TTTGGGCTGCCCTGTGTGCTGAGAGTGTACAAAAG 362	
RESULT	3		
AW326901			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
AW326901 433 bp mRNA EST 27-JAN-2000 20104 MARC 2BOV Bos taurus CDNA 5', mRNA sequence. AW326901 GI:6762822 EST. SOURCE Bos taurus. ORGANISM Bos taurus Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. 1 (bases 1 to 433) Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and Keele,J.W. Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle Unpublished (2000) On Dec 20, 1995 this sequence version replaced gi:1133576. Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -mismatch 12 options. PCR Primers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTCCAGCTACGACG Plate: 10 row: G column: 24 Seq primer: ATTAGTGACACTATAG. Location/Qualifiers 1..433 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="MARC 2BOV" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semiteadonous muscle, longissimus muscle, pancreas, adrenal, and endometrium." BASE COUNT 80 a 142 c 143 g 68 t ORIGIN			
Query Match	44.2%;	Score 257.6;	DB 80; Length 433;
Best Local Similarity	95.0%;	Pred. No. 3.1e-50;	
Matches 266;	Conservative 0;	Mismatches 14;	Indels 0; Gaps 0;
QY	1	atggcgacccagctcgcccccagacacacagggtctgtgtggcagactttgtaggttat	60
Db	154	ATGGCAGCCCCAGCCTCGGCCCCAGACACACGGGTCTAGTGGCAGACTTTGTGGCTAT	213

No.	Score	Match	Length	DB	ID	Description
1	357.2	61.3	540	79	AW258810	um74a02.y
2	288	44.2	362	35	AA596919	2012f08.i
3	257.6	44.2	433	80	XA326901	20104.MAR
4	160.6	27.5	416	71	WN159063	2a50h02.x
5	136.8	26.9	431	64	AW048567	UI-M-BH1
6	152	26.1	628	108	AQ032175	RPCI-11-3
7	148.8	25.5	549	109	AQ650588	HS_5340_B
8	135.6	23.3	455	106	AQ401160	HS_5062_A
9	125.8	21.6	404	51	AI1716839	R-YO-a
10	119.4	20.5	584	79	AL134785	UI-M-BH2
11	116.6	20.0	454	69	AW124015	UI-M-BH2
12	114.6	19.7	535	40	AA939725	v292a11.r
13	114.2	19.6	437	25	W01420	za73g06.r
14	111.2	19.1	471	46	AA1041297	t992c06.x
15	109.6	18.8	299	21	F08773	HSC25B061.n
16	108.8	18.7	472	43	AI180733	UI819073
17	104.6	17.9	471	34	AA509753	vb52c06.r
18	76.6	13.1	1696	83	AF149300	Rattus.no
19	53.8	9.2	574	81	AW418903	Est15d05.x
20	52.8	9.1	274	20	T29044	hs16g242.Hu
21	52.6	9.0	516	22	H09884	ym05b07.r
22	51.8	8.9	714	64	AW072826	xa42e07.x
23	50.2	8.6	640	40	AA981864	ua36g07.r
24	49	8.4	478	61	AI7837675	UI-M-AK0-
25	49	8.4	497	27	AA016399	mc88g02.r
26	47.6	8.2	540	44	AI326919	mj39b01.x
27	47.6	8.2	624	44	AI323521	mo57b02.x
28	47.4	8.1	547	41	AI020744	ub01h12.r
29	47	8.1	418	34	AA458294	vg48c03.r
30	46.6	8.0	616	44	AI323048	mj41h10.y
31	46.4	8.0	534	44	AI322704	mj39b01.y
32	46.4	8.0	545	26	W42014	mb16g04.r
33	46.4	8.0	562	27	AA015184	mh33d12.r
34	45.8	7.9	592	27	AA051441	mj41h10.r
35	45.8	7.9	616	26	W97433	mp95f12.r
36	45.4	7.8	747	74	AW226585	uf03f12.x
37	45.4	7.8	776	82	CNS010RY	AA093352
38	45.4	7.8	925	82	CNS0091P	Drosophil
39	45.2	7.8	925	82	CNS0091P	AL053013
40	45.2	7.8	1101	83	CNS0153F	Drosophil
41	45.2	7.8	1101	83	CNS01684	AL107098
42	44.8	7.7	446	27	AA049970	mj39b01.r
43	44.8	7.7	1101	83	CNS016MA	AI106924
44	44.6	7.7	1084	83	CNS0156D	AL105055
45	43.8	7.5	997	82	CNS006DN	AI065132

ALIGNMENTS

RESULT	1
AWA258810	
LOCUS	
DEFINITION	un74a02.y1 Sugano mouse kidney mkoa Mus musculus cDNA clone IMAGE:2300906 5' similar to SW:BCIW_MOUSE P70345 APOPTOSIS REGULATOR BCL-W. [2] SW:BCIW_MOUSE ;, mRNA sequence.
ACCESSION	AW258810
VERSION	AW258810.1
KEYWORDS	GI:6631791
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M.,Weising,B., Allen,M., Boxers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E., Korn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson.R. The WashU-NCI Mouse EST Project 1999 Unpublished (1999)
TITLE	
JOURNAL	

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OM nucleic - nucleic search, using sw model

Run on: July 3, 2000, 20:30:41 ; Search time 795.04 Seconds
(without alignments)
2972.214 Million cell updates/sec

Title: US-09-155-327B-6
Perfect score: 583
Sequence: 1 atggcagcccccagcctcgge.....ctttttgctagcaagttaa 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
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11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
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74: gb_est44:*
75: em_est31:*
76: em_est32:*
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78: em_est34:*
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86: em_gss1:*
87: em_gss2:*
88: em_gss3:*
89: em_gss4:*
90: gb_gss5:*
91: gb_gss6:*
92: gb_gss7:*
93: gb_gss8:*
94: gb_gss9:*
95: em_gss5:*
96: em_gss6:*
97: em_gss7:*
98: em_gss8:*
99: em_gss9:*
100: em_gss10:*
101: em_gss11:*
102: gb_gss10:*
103: gb_gss11:*
104: em_gss12:*
105: gb_gss12:*
106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96178771.
 RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.;
 RT "The E1B 19K protein blocks apoptosis by interacting with and
 RT inhibiting the p53-inducible and death-promoting Bax protein.";
 RL Genes Dev. 10:461-477(1996).
 RN [2]
 RP SEQUENCE OF 75-192 FROM N.A.
 RX TISSUE=BRAIN;
 RC MEDLINE; 97147318.
 RA Madison D.L., Pfeiffer S.E.;
 RT "Cloning of the 3' end of rat bax-alpha and corresponding
 RT developmental down-regulation in differentiating primary, cultured
 RT oligodendrocytes";
 RL Neurosci. Lett. 220:183-186(1996).
 RN [3]
 RP SEQUENCE OF 37-169 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE; 95129487.
 RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 RT cell apoptosis is associated with decreased bax and constitutive
 RT bcl-2 and bcl-x long messenger ribonucleic acid levels.";
 RL Endocrinology 136:232-241(1995).
 CC -1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
 CC -1- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO
 CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
 CC HIGHEST LEVELS IN THE TESTIS AND OVARY.
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR
 CC THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 DR EMBL; 226528; CAB1299.1; -;
 DR EMBL; U59184; AAC5298.1; -;
 DR EMBL; U32098; AAA75200.1; -;
 DR EMBL; U67511; AAC60700.1; -;
 DR EMBL; U49729; AAC26327.1; -;
 DR HSP; P53563; IAF3.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS50062; BCL2 FAMILY; 1.
 DR PFAM; PF00452; Bcl-2; 1.
 KW Apoptosis; Transmembrane; Alternative splicing.
 FT DOMAIN 59 73 BH3.
 FT DOMAIN 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT TRANSMEM 172 192 POTENTIAL.
 FT CONFLICT 72 72 S -> N (IN REF. 3).
 FT

FT CONFLICT 76 76 L -> M (IN REF. 2).
 FT CONFLICT 126 126 C -> Y (IN REF. 2).
 FT CONFLICT 149 149 L -> F (IN REF. 3).
 FT CONFLICT 159 159 D -> E (IN REF. 1).
 SQ SEQUENCE 192 AA; 21350 MW; 7B3CDI98D56DF589 CRC64;
 Query Match 16.5%; Score 231; DB 1; Length 192;
 Best Local Similarity 27.3%; Pred. No. 4.44e-25;
 Matches 33; Conservative 36; Mismatches 47; Indels 5; Gaps 4;
 Db 50 PPQDASTKKLSECLRRIGDELDLSNM--ELQRMIAVDV-T-DSPREVFRVAADMFDGDNF 105
 Qy 33 PGEGPAADPLHOAMRAAGDEFEFRRTTSDLAALHWTGSAQORFTQVSDLEFQGGP- 91
 Db 106 NWRGVVALFFASKLVLKALCTKYPELIRITMGWTLDFLRERLLVWIDODGGWGLLSYF 165
 Qy 92 NWGRLVAFLLFGAALCAESVKNKEPLVGQVQEMVVAILETRLDVWTHSSGGWGAETALY 151
 Db 166 G 166
 Qy 152 G 152
 RESULT 15
 ID BAXA_MOUSE STANDARD; PRT; 192 AA.
 AC Q07813;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
 GN BAX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X DBA/2;
 RX MEDLINE; 93364978.
 RA Oltvai Z.N., Millman C.L., Korsmeyer S.J.;
 RT "bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
 RT accelerates programmed cell death.";
 RL Cell 74:609-619(1993).
 CC -1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
 CC LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
 CC CESSATION OF SPERM PRODUCTION.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
 CC -1- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO
 CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR
 CC THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC -----
 DR EMBL; L22472; AAA03622.1; -;
 DR HSP; P53563; IAF3.
 DR

RESULT 13

RESULT		14	
ID	BAXA-RAT	STANDARD;	PRT; 192 AA.
AC	Q63690; Q62995;	Q64383;	
DT	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DT	15-FEB-2000	(Rel. 39, Last annotation update)	
DE	APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.		
DD	BAX.		
GN	Rattus norvegicus (Rat).		
OS	BAX.		

DR PROSITE; PS00063; BH4.2; 1.
 DR PFAM; PF00452; Bcl-2; 1.
 KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
 FT 3D-structure.
 FT DOMAIN 4 24 BH4.
 FT DOMAIN 86 100 BH3.
 FT DOMAIN 129 148 BH1.
 FT DOMAIN 180 195 BH2.
 FT TRANSMEM 210 226
 FT VARSPIC 126 188
 FT VARSPIC 189 233
 FT
 FT CONFLICT 6 6
 FT CONFLICT 12 12
 FT CONFLICT 64 64
 FT CONFLICT 81 81
 FT CONFLICT 119 119
 FT CONFLICT 143 144
 FT CONFLICT 199 199
 FT CONFLICT 201 201
 FT SEQUENCE 233 AA; 26158 MW; 2862B6C63864BC8F CRC64;
 Query Match 44.0%; Score 615; DB 1; Length 233;
 Best Local Similarity 53.1%; Pred. NO. 5.42e-110;
 Matches 77; Conservative 30; Mismatches 36; Indels 2; Gaps 2;
 Db 85 AVKQALRAGDEFEFLRYRFRSDLTSLQHTPTGAYQSFQVYVNEFLFRDGVNMGRIYVAF 144
 Qy 41 PLHQMARAGDEFEFLRYRFRSDLTSLQHTPTGAYQSFQVYVNEFLFRDGVNMGRIYVAF 100
 Db 145 SFGGALCVESYDKEMQVLVSRIASWATYLNHLEPITQENGWDTFVLYLGNNAAESR 204
 Qy 101 LFGAALCAESYKEMQVLVSRIASWATYLNHLEPITQENGWDTFVLYLGNNAAESR 160
 Db 205 KQERFNRWFLTGMVAGVLLGLS 229
 Qy 161 RLREG-N-WASVRLTGAVALGAL 183
 RESULT 8
 ID BCLX_MOUSE STANDARD; PRT; 233 AA.
 AC Q64373; Q60657; Q60658; Q61338;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE APOPTOSIS REGULATOR BCL-X.
 GN BCL2L1 OR BCL2L OR BCLX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2A4B;
 RA Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
 RC STRAIN=C57BL/6; TISSUE=BRIN;
 RX MEDLINE; 95331139.
 RA Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L., Boise L.H.,
 Thompson C.B., Nunez G.;
 RT "bcl-XL is the major bcl-x mRNA form expressed during murine
 development and its product localizes to mitochondria.";
 RL Development 120:3033-3042(1994).
 RN [3]
 RP SEQUENCE FROM N.A. (X(L); X(S) AND X(DELTA-TM) ISOFORMS).
 RC TISSUE=PRE-B CELL;
 RX MEDLINE; 95052604.
 RA Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
 RT "Cloning and molecular characterization of mouse bcl-x in B and T
 lymphocytes.";
 RL J. Immunol. 153:4388-4398(1994).

[4]
 RP SEQUENCE FROM N.A. (BETA ISOFORM).
 RC STRAIN=C57BL/6 X CBA; TISSUE=THYMUS;
 RX MEDLINE; 98051053.
 RA Yang X.-F., Weber G.F., Cantor H.;
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates
 apoptosis in T cells.";
 RL Immunity 7:629-639(1997).
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97289584.
 RA Grillo D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
 Ohta S., Seldin M.F., Nunez G.;
 RT "Genomic organization, promoter region analysis, and chromosome
 localization of the mouse bcl-x gene.";
 RL J. Immunol. 158:4750-4757(1997).
 CC -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
 FORM AND THE DELTA-TM FORM DISPLAY CELL DEATH REPRESSOR ACTIVITY,
 WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
 CC -!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
 BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
 BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
 SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
 ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
 CC -!- ALTERNATIVE PRODUCTS: FOUR ISOFORMS, BCX-X(L) (SHOWN HERE), BCL-
 X(S), BCL-X-BETA AND BCL-X(DELTA-TM), ARE DERIVED BY ALTERNATIVE
 SPLICING.
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE
 BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-
 TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
 ACTIVATED.
 CC -!- DEVELOPMENTAL STAGE: BCL-X(BETA) IS EXPRESSED IN BOTH EMBRYONAL AND
 POSTNATAL TISSUES.
 CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
 FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
 APOPTOTIC ACTIVITY (BY SIMILARITY).
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 4 (BH4).
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC
 CC EMBL; X83574; CAA58557.1; -
 CC EMBL; L35049; AAA51039.1; -
 CC EMBL; L35048; AAA51040.1; -
 CC EMBL; U10102; AAA82174.1; -
 CC EMBL; U10101; AAA82173.1; -
 CC EMBL; U10100; AAA82172.1; -
 CC EMBL; U51279; AAC53460.1; -
 CC EMBL; U78031; AAB96881.1; -
 CC EMBL; U78030; AAB96881.1; JOINED.
 CC HSSP; P53563; IAF3.
 CC MGD; MGI:88139; BCL2L.
 CC PROSITE; PS50062; BCL2_FAMILY; 1.
 CC PROSITE; PS01080; BH1; 1.
 CC PROSITE; PS01258; BH2; 1.
 CC PROSITE; PS01259; BH3; 1.
 CC PROSITE; PS01260; BH4_1; 1.
 CC PROSITE; PS50063; BH4_2; 1.
 CC PFAM; PF00452; Bcl-2; 1.
 KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
 FT DOMAIN 4 24 BH4.
 FT DOMAIN 86 100 BH3.

CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
 CC ENVELOPE (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT
 CC ISOFORM ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
 CC DEVELOPMENT.
 CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
 CC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
 CC APOPTOTIC ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 4 (BH4).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC EMBL; 223110; CAAB0657.1; -.
 CC EMBL; U26645; AAB07677.1; -.
 CC PIR; A47537; A47537.
 CC HSP; P53563; 1AF3.
 CC PROSITE; PS00062; BCL2_FAMILY; 1.
 CC PROSITE; PS01080; BH1; 1.
 CC PROSITE; PS01258; BH2; 1.
 CC PROSITE; PS01259; BH3; 1.
 CC PROSITE; PS01260; BH4; 1.
 CC PROSITE; PS00063; BH4_2; 1.
 CC PFAM; PF00452; Bcl-2; 1.
 CC Apoptosis; Transmembrane; Alternative splicing.
 KW DOMAIN 4 24
 FT DOMAIN 82 96
 FT DOMAIN 125 144
 FT DOMAIN 176 191
 FT TRANSMEM 206 223
 FT VARSPIC 185 229
 FT ERFVLYGNAAELRGQETFNKWLITGATVAGVLLGSL
 FT LSRK -> VRTALP (IN SHORT ISOFORM).
 SQ SEQUENCE 229 AA; 25733 MW; A37D3A4D0C0E9DA CRC64;
 Query Match 44.0%; Score 615; DB 1; Length 229;
 Best Local Similarity 52.3%; Pred. No. 5,42e-110;
 Matches 78; Conservative 30; Mismatches 39; Indels 2; Gaps 2;
 Db 79 ASDVROALRDAGDEFELRYRAFSDLTSQLHITPGTAYQSFQVNVNLFHDPGVNMGRIVA 138
 QY 39 ADPLHQAMRAAGDEFETFRRTFSDLAALQHVTPGSAQQRFTQVSDLELFGGPNWGRILVA 98
 Db 139 FFSFGALCVESVDKEMRVLCGRIVSWMTYLTDLDPWIGENGWERFVLYGNNAAE 198
 QY 99 FFLFGAALCAESVKNEMPLEVQGVQWVMVAYLETRLDVHIHSSGGWAEFTALYGDGALEE 158
 Db 199 LRKQGTENKLLTGTAVGVLLGLSLS 227
 QY 159 ARRLREG-N-WASVRTVLITGAVALGALVT 185
 RESULT 7
 ID BCLX RAT STANDARD; PROT; 233 AA.
 AC P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128;
 DT 01-Oct-1996 (Rel. 34, Created)
 DT 01-Nov-1997 (Rel. 35, Last sequence update)
 DT 01-Nov-1997 (Rel. 35, Last annotation update)
 DE APOPTOSIS REGULATOR BCL-X.
 GN BCL2L1 OR BCL2L OR BCLX.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]

RP SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
 RC TISSUE-BRAIN;
 RA Michaelidis T.M.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Wesselindh S.L.; Choi S.; Veliuona M.; Hardwick J.M.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
 RC TISSUE-THYMUS;
 RX MEDLINE; 96278736.
 RA Shiraiwa N.; Inohara N.; Okada S.; Yuzaki M.; Shoji S.-I.; Ohta S.;
 RT "An additional form of rat bcl-x. Bcl-xbeta, generated by an
 RT unspliced RNA, promotes apoptosis in promyeloid cells.";
 RL J. Biol. Chem. 271:13258-13265(1996).
 [4]
 RP SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
 RX MEDLINE; 95129487.
 RA Tilly J.L.; Tilly K.I.; Kenton M.L.; Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 RT cell apoptosis is associated with decreased bax and constitutive
 RT bcl-2 and bcl-x-long messenger ribonucleic acid levels.";
 RL Endocrinology 136:232-241(1995).
 CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
 CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT AND
 CC THE BETA ISOFORMS PROMOTE APOPTOSIS.
 CC -1- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
 CC BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
 CC BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
 CC ENVELOPE (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS, BCL-X(L) (SHOWN HERE),
 CC BCL-X(S) AND BCL-X(BETA), ARE DERIVED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
 CC SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
 CC OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
 CC DETECTABLE LEVEL OF BCL-X(S).
 CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
 CC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
 CC APOPTOTIC ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 4 (BH4).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC -----
 CC EMBL; X82537; CAA57886.1; -.
 CC EMBL; X82537; CAA57887.1; -.
 CC EMBL; U10579; AAA19257.1; -.
 CC EMBL; U72350; AAB17353.1; -.
 CC EMBL; U72349; AAB17352.1; -.
 CC EMBL; U34963; AAC77686.1; -.
 CC EMBL; S76513; AAC60701.1; ALT_INIT.
 CC EMBL; S78284; AAC60702.1; -.
 CC PDB; 1AF3; 07-JUL-97.
 CC PROSITE; PS00062; BCL2_FAMILY; 1.
 CC PROSITE; PS01080; BH1; 1.
 CC PROSITE; PS01258; BH2; 1.
 CC PROSITE; PS01259; BH3; 1.
 CC PROSITE; PS01260; BH4_1; 1.

[illegible]

CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLGY DOMAIN 2 (BH2).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----

DR EMBL: X82462; CAA57845.1; -
 DR HSP: P53563; IAF3.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS50062; BCL2 FAMILY; 1.
 DR PFAM: PF00452; Bcl-2; 1.
 KW Apoptosis; Transmembrane.
 FT DOMAIN 1 1
 FT DOMAIN 120 139 BH1.
 FT DOMAIN 171 186 BH2.
 FT TRANSMEM 207 227 POTENTIAL.
 SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 66.6%; Score 931; DB 1; Length 228;
 Best Local Similarity 67.9%; Pred. No. 3.73e-184;
 Matches 125; Conservative 35; Mismatches 21; Indels 3; Gaps 2;

Db 48 SRALVEDLVYKLCQSLV--PPFS-CAASCALHSAMRAAGDEFEFRFQAISEISTQIH 104
 QY 10 TRALVADFVGYKURQYVCGAGGPGGAADPLHQAMRAAGDEFEFRFRFTSDLAALQH 69
 Db 105 VTPGTAYARFAEAVAGSLFGGWNWGRIVAFVFGAALCAESVKNKMSPLLPRIQDMVMTY 164
 QY 70 VTPGSAQQRFTQVSDLEFGGPNWGRVLAFFLFGAALCAESVKNKMEPLVGQVQEMWVAY 129
 Db 165 LETNLRDWTOSNGWNGFTLYGDGAIEARQREGNWSLTKTLTGAVAGALMTVGAL 224
 QY 130 LETRLVDWTHSSGGWAEFTLYGDGALEARRREGNWSVRLTGTGAVAGALVTVGAF 189
 Db 225 FASK 228
 QY 190 FASK 193

RESULT 4
 ID BCLX_PIG STANDARD; PRT; 233 AA.
 AC O7737.
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE APOPTOSIS REGULATOR BCL-X.
 GN BCL2L1 OR BCL2L OR BCLX.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
 RT "Expression of apoptosis-associated genes in hibernating and stunned
 RT myocardium of pig."
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
 CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT AND
 CC THE BETA ISOFORMS PROMOTE APOPTOSIS.
 CC -1- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
 CC BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
 CC BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
 CC ENVELOPE (BY SIMILARITY).
 CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
 CC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-

CC APOPTOTIC ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLGY DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLGY DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLGY DOMAIN 3 (BH3).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLGY DOMAIN 4 (BH4).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----

DR EMBL: AJ001203; CAA04597.1; -
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4_1; 1.
 DR PROSITE: PS50063; BH4_2; 1.
 DR PFAM: PF00452; Bcl-2; 1.

KW Apoptosis; Mitochondrion; Transmembrane.
 FT DOMAIN 4 24
 FT DOMAIN 86 100 BH4.
 FT DOMAIN 129 148 BH3.
 FT DOMAIN 180 195 BH1.
 FT TRANSMEM 210 226 BH2.
 SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 44.2%; Score 618; DB 1; Length 233;
 Best Local Similarity 53.8%; Pred. No. 1.10e-110;
 Matches 78; Conservative 29; Mismatches 36; Indels 2; Gaps 2;

Db 85 AVKQALREAGDEFELRYRRAFSDLTSQLHTPTGAYQSFQVLNLFQDGVNMGRIVAFF 144
 QY 41 PLHQAMRAAGDEFERFRRTSDLAALQHLVTPGSAQQRFTQVSDLEFGGPNWGRVLAFF 100
 Db 145 SFGALCVESVDKEMQVLVSRIATWMTATYLNHLEPWIQENGWMDTFVELYGNNAAESR 204
 QY 101 LFGAALCAESVKNKMEPLVGQVQEMVAYLETRLVDWIHSSGGWAEFTLYGDGALEAR 160
 Db 205 KQQRFNRFNLTGMTLAGVLLGSL 229
 QY 161 RLREG-N-WASVRLTGTGAVAGAL 183

RESULT 5
 ID BCLX_HUMAN STANDARD; PRT; 233 AA.
 AC Q07817; O92976;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE APOPTOSIS REGULATOR BCL-X.
 GN BCL2L1 OR BCL2L OR BCLX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
 RX MEDLINE; 93364977.
 RA Boile L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
 RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
 RT of apoptotic cell death."
 RL Cell 74:597-608(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (BETA ISOFORM).
 RA Inohara N., Ohta S.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:14:40 2000; MasPar time 7.84 Seconds
Tabular output not generated. 749.617 Million cell updates/sec

Title: >US-09-155-327B-7
Description: (1-193) from US09155327B.pep
Perfect Score: 1397
Sequence: 1 MATPASAPDTRALVADEFVGY.....LTGVALGALVTYGAFFASK 193

Scoring table: PAM 150
Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 46.104; Variance 80.361; scale 0.574

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Description	ID	Pred. No.
1	1383	99.0	APOPTOSIS REGULATOR BC	1 BCLW_HUMAN	2.09e-292
2	1380	98.8	APOPTOSIS REGULATOR BC	1 BCLW_MOUSE	1.10e-291
3	931	66.6	APOPTOSIS REGULATOR R1	1 ARL1_XENLA	3.73e-184
4	618	44.2	APOPTOSIS REGULATOR BC	1 BCLX_PIG	1.10e-110
5	616	44.1	APOPTOSIS REGULATOR BC	1 BCLX_HUMAN	3.18e-110
6	615	44.0	APOPTOSIS REGULATOR BC	1 BCLX_CHICK	5.42e-110
7	615	44.0	APOPTOSIS REGULATOR BC	1 BCLX_RAT	5.42e-110
8	615	44.0	APOPTOSIS REGULATOR BC	1 BCLX_MOUSE	5.42e-110
9	587	42.0	APOPTOSIS REGULATOR BC	1 BCL2_CHICK	1.57e-103
10	586	41.9	APOPTOSIS REGULATOR BC	1 BCL2_RAT	2.68e-103
11	586	41.9	APOPTOSIS REGULATOR BC	1 BCL2_HUMAN	2.68e-103
12	584	41.8	APOPTOSIS REGULATOR BC	1 BCL2_MOUSE	7.73e-103
13	554	39.7	APOPTOSIS REGULATOR R1	1 ARL1_XENLA	6.05e-96
14	231	16.5	APOPTOSIS REGULATOR BA	1 BAXA_RAT	4.44e-25
15	231	16.5	APOPTOSIS REGULATOR BA	1 BAXA_MOUSE	4.44e-25
16	229	16.4	APOPTOSIS REGULATOR BA	1 BAXA_BOVIN	1.12e-24
17	228	16.3	APOPTOSIS REGULATOR BA	1 BAXD_HUMAN	1.78e-24
18	228	16.3	APOPTOSIS REGULATOR BA	1 BAXD_HUMAN	1.78e-24
19	226	16.2	BCL-2 HOMOLOGOUS ANTAG	1 BAK_HUMAN	4.50e-24
20	225	16.1	BCL-2 HOMOLOGOUS ANTAG	1 BAK_HUMAN	7.14e-24
21	218	15.6	APOPTOSIS REGULATOR BA	1 BAXB_HUMAN	1.79e-22
22	210	15.0	BCL-2 HOMOLOGOUS ANTAG	1 BAK_MOUSE	6.86e-21
23	183	13.1	APOPTOSIS REGULATOR NR	1 NR13_COTJA	1.15e-15

24	156	11.2	1	CED9_CAEBR	APOPTOSIS REGULATOR CE	1.11e-10
25	155	11.1	1	BELL_MOUSE	BCL2-RELATED PROTEIN A	1.68e-10
26	149	10.7	1	BCL1_HUMAN	INDUCED MYELOID LEUKEM	1.95e-09
27	150	10.7	1	MCL1_HUMAN	INDUCED MYELOID LEUKEM	1.30e-09
28	148	10.6	1	CED9_CAEBL	APOPTOSIS REGULATOR CE	2.93e-09
29	131	9.4	1	EAR_ASFE4	APOPTOSIS REGULATOR BC	2.38e-06
30	130	9.3	1	EAR_ASFM2	APOPTOSIS REGULATOR BC	3.49e-06
31	130	9.3	1	EAR_ASFB7	APOPTOSIS REGULATOR BC	3.49e-06
32	98	7.0	1	NOL0_RHISN	MODULATION PROTEIN NOL	2.93e-01
33	95	6.8	1	YH70_SYNY3	HYPOHETICAL 67.1 KD P	7.61e-01
34	93	6.7	1	LIGC_TRAVE	LIGNINASE C PRECURSOR	1.42e-00
35	94	6.7	1	EXG_YARLI	GLUCAN 1,3-BETA-GLUCOS	1.42e-00
36	93	6.7	1	DINF_ECOLI	DNA-DAMAGE-INDUCIBLE P	1.42e-00
37	94	6.7	1	GAG_FV2G1	GAG POLYPROTEIN (CONTA	1.04e-00
38	94	6.7	1	Y4FN_RHISN	PROBABLE ABC TRANSPORT	1.04e-00
39	94	6.7	1	LRPL_CHICK	LOW-DENSITY LIPOPROTEI	1.04e-00
40	92	6.6	1	YH28_YEAST	HYPOHETICAL 36.5 KD P	1.93e-00
41	92	6.6	1	ARAA_SALTY	L-ARABINOSIDE ISOMERASE	1.93e-00
42	92	6.6	1	MEFD_HUMAN	MYOCYTE-SPECIFIC ENHAN	1.93e-00
43	92	6.6	1	COMA_NEIGO	COMPETENCE PROTEIN COM	1.93e-00
44	92	6.6	1	PULA_THEMA	PULULANASE PRECURSOR	1.93e-00
45	92	6.6	1	HELY_MYCTU	PUTATIVE HELICASE HELY	1.93e-00

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	193 AA.
ID	BCLW_HUMAN	Q92843;		
AC	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	APOPTOSIS REGULATOR BCL-W (K1AA0271).			
GN	BCL2L2 OR BCLW.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 96358615.			
RA	Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,			
RA	Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;			
RA	"bcl-w, a novel member of the bcl-2 family, promotes cell survival.";			
RL	Oncogene 13:665-675(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 97191544.			
RA	Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,			
RA	Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;			
RT	"Prediction of the coding sequences of unidentified human genes. VI.			
RT	The coding sequences of 80 new genes (K1AA0201-K1AA0280) deduced by			
RT	analysis of cDNA clones from cell line KG-1 and brain.";			
RL	DNA Res. 3:321-329(1996).			
CC	-1- FUNCTION: PROMOTES CELL SURVIVAL.			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND			
CC	IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,			
CC	AND SALIVARY GLAND.			
CC	-1- DOMAIN: B44 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC			
CC	FUNCTION.			
CC	-1- SIMILARITY: CONTAINS A BCL-2 HOMOLGY DOMAIN 1 (BH1).			
CC	-1- SIMILARITY: CONTAINS A BCL-2 HOMOLGY DOMAIN 2 (BH2).			
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			
CC	-----			
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viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbci-y and Hbci-y may have span such as cancer conditions associated with prolonged cell life span such as cancer (especially Kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.

Query Match	95.7%	Score 1326;	DB 1;	Length 192;
Best Local Similarity	94.3%;	Pred. No. 7,33e-117;		
Matches	181;	Conservative	8;	Mismatches 2; Indels 1; Gaps 1;
Db	1	ATPASPDTRALYEDFVGYYKLROKGYVCGAGPCEGPAADPLHQAMRAAGDEFEFTRFRRTF	60	
QY	2	PTPASFPDTRALYADFVGYYLRLROKGYVCGAGPCEGPAADPLHQAMRAAGDEFEFTRFRRTF	61	
Db	61	SDLAAQLHVTTPGSAQORFTOVSDLEFQGGPNWGLRVAFVFGGAALCAESYNKEMEPLVGQ	120	
QY	62	SDLAAQLHVTTPGSAQORFTOVSDLEFQGGPNWGLRVAFVFGGAALCAESYNKEMEPLVGQ	121	
Db	121	VQEWVYALFTRLADWTHSSGGWAEFTALYCDGCALEARRLRGNWASVRTVLVTGVAALG	180	
QY	122	VQDWIVAYLFTRLADWTHSSGGWADFTALYCDGCALEARRLRGNWA-VSTVVTGVAALG	180	
Db	181	ALVTVGGAFFASK	192	
QY	181	ALVTVGGAFFASK	192	

RESULT 12

ID W36048 standard; Protein; 168 AA.
AC W36048;
DT 22-APR-1998 (first entry)
DE Mouse bcl-w protein.
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
OS MUS SP;
PN W0975971-AL.
PD 02-OCT-1997.
PF 27-MAR-1997; AU0199.
PR 27-MAR-1996; AU-008965.
PT (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Adams JM, Cory S, Gibson LM, Holmgren SP;
DR WPI: 97-489635/45.
DR N-PSDB: T96578.
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases
PS Claim 6; Page 50-51; 86pp; English.
CC This sequence represents a novel protein, bcl-w, encoded by the mouse
CC bcl-2 gene family. This gene promotes cell survival, so its modulation
CC is useful in treatment of cancer or auto-immune diseases, degenerative
CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
CC or in cell transplants. Up-regulation of the gene can also be used to
CC modify cell lines cultured *in vivo*, e.g. to develop new lines, to
CC facilitate isolation of hybridomas and to increase survival of primary
CC explants during genetic modification. It can be used to produce
CC recombinant Bcl-w for therapy, diagnosis, antibody production or
CC screening of potential modulators.
SQ Sequence 168 AA;

	Query Match	89.1%	Score 1235,	DB 1:	Length 168;
	Best Local Similarity 100.0%;	Pred. No. 7.82e-108;	Mismatches 0;	Indels 0;	Gaps 0;
	Matches 168;	Conservative			
Db	1	MPTASTPDTRALVADVGYRLRKGVCAGGEGPAADPLHOAMRAAGDEETFRRT	60		
Qy	1	MPTASTPDTRALVADVGYRLRKGVCAGGEGPAADPLHOAMRAAGDEETFRRT	60		
Db	61	FSDLAALHVTTPGSAORQFTQVSDLPFGGPNNGRLVAFVFGAALCAESVNMEMPVG	120		
Qy	61	FSDLAALHVTTPGSAORFTQVSDLPFGGPNNGRLVAFVFGAALCAESVNMEMPVG	120		

Db	121	QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLRGNWA	168
QY	121	QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLRGNWA	168
RESULT	13		
ID	W59884	standard; Protein; 365 AA.	
AC	W59884;		
DE	20-NOV-1998	(first entry)	
DT	DE	Amino acid sequence of the cDNA clone Bcl-like (HAICH29).	
KW	Bcl-like (HAICH29);	chronic inflammatory disease; allergic reaction;	
KW	immunological disorder;	autoimmune disease; anti-infectious agent.	
OS	Homo sapiens.		
PN	WO9831800-A2.		
PD	23-JUL-1998.		
PF	21-JAN-1998;	U00960.	
PR	21-JAN-1997;	US-034205.	
PR	21-JAN-1997;	US-034204.	
PA	(AUCC-) AUCLAND UNISERVICES LTD.		
PA	(HUMA-) HUMAN GENOME SCI INC.		
PI	Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,		
PI	Su JY;		
DR	WPI; 98-414099/35.		
DR	N-PSDB; V41925.		
PT	New Isolated polynucleotides and encoded polypeptides - used to		
PT	develop products for treating e.g. inflammatory diseases,		
PT	infections, immunological disorders, autoimmune diseases, allergies		
PT	or tumours		
FS	Claim 1; Fig 12A-12D; 120pp; English.		
CC	This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),		
CC	used in the method of the invention. The products of the clone can be		
CC	used for treating conditions associated with abnormal expression of		
CC	the polypeptides. They can be used for e.g. treating chronic		
CC	inflammatory diseases, immunological disorders, autoimmune diseases,		
CC	inflammatory diseases, various allergies, and as anti-infectious agents.		
CC	The products can also be used for detection and diagnosis.		
SO	Sequence	365 AA;	

[illegible]

RESULT	14
ID	W19396 standard; protein; 225 AA.
AC	W19396;
DT	05-MAR-1998 (first entry)
DE	"Deprenyl" (RTM)-induced protein 1.
DE	"Deprenyl" (RTM)-induced protein; neuroactive drug; neuronal cell; apoptosis;
KW	Deprenyl-induced protein; neuroactive drug; neuronal cell; apoptosis;
KW	neurodegenerative disorder; oligodendrocyte; multiple sclerosis.
OS	Rattus rattus.
PN	W09725421-A2.
PN	17-JUL-1997.
PD	
PF	21-DEC-1996; E05800.
PR	12-JAN-1996; GB-000660.
PA	(NOVS) NOVARTIS AG.
PI	Furst P, Tatton WG, Waldmeier P;
DI	WPI; 97-384980/35.
DR	
PT	New isolated "Deprenyl" (RTM)-induced
PT	products for use in the diagnosis and treatment of neural disorders,
pt	

KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
 KW animal model.
 OS Homo sapiens.
 PN NC9913710-A1.
 PD 23-MAR-1999.
 PF 16-SEP-1997; AU-009228.
 PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA Adams J, Cory S, Gibson L, Koentgen F, Print C;
 PI WPI: 99-243890/20.
 DR N-PSDB; X25134.
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w

PS Disclosure: Page 37: 52pp; English.
 CC The present sequence is described of a derivative of human Bcl-w
 CC (see also X05530), a pro-survival member of the Bcl-2 family that
 CC is widely expressed and which is essential for spermatogenesis.
 CC The invention relates generally to a method of treatment and to an
 CC animal model for the identification of molecules and genetic
 CC sequences useful for inducing or reducing fertility of male animals.
 CC Methods are provided for the treatment of infertility, or for
 CC reducing fertility, by modulating spermatogenesis. An animal model
 CC carries a mutation in at least one allele of the human or murine
 CC Bcl-w gene (see X25132-35) or in a gene associated with Bcl-w.
 CC Such animals have disorganised seminiferous tubules and are
 CC substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to
 CC screen for therapeutic molecules including genetic sequences
 CC capable of inducing, enhancing or otherwise facilitating
 CC spermatogenesis in animals, or which can induce infertility.
 CC Sequence 193 AA;

Query Match 96.0%; Score 1331; DB 1; Length 193;
 Best Local Similarity 93.8%; Pred. No. 2.34e-117;
 Matches 181; Conservative 9; Mismatches 2; Indels 1; Gaps 1;

Db 1 MATPASAPDTRALVADVGVYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETFRRT 60
 QY 1 MPTPASTPTDTRALVADVGVYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETFRRT 60
 Db 61 FSDLAALQHLVTPGSAQQRFTQVSDLEFQGGPNWGRVLAFFLFGAALCAESYNKEMEPLVG 120
 QY 61 FSDLAALQHLVTPGSAQQRFTQVSDLEFQGGPNWGRVLAFFLFGAALCAESYNKEMEPLVG 120
 Db 121 QVQEMWVAYLETRLDVNIHSSGGWAEFTALYGDGAEARLRREGNWSVTVLTGAVAL 180
 QY 121 QVQDMIVAYLETRLDVNIHSSGGWAEFTALYGDGAEARLRREGNWSVTVLTGAVAL 179
 Db 181 GALVTGGAFFASK 193
 QY 180 GALVTGGAFFASK 192

RESULT 10

ID W36047 standard; Protein; 193 AA.
 AC W36047;
 DE Human bcl-w protein.
 KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 KW diagnosis; degenerative disease.
 OS Homo sapiens.
 PN WO9735971-A1.
 PD 02-OCT-1997.
 PF 27-MAR-1997; AU0199.
 PR (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA Adams JM, Cory S, Gibson LM, Holmgren SP;
 PI WPI: 97-489635/45.
 DR N-PSDB; T96577.
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
 PT or inhibit cell survival, e.g. for treatment of cancer and
 PT degenerative diseases
 PS Claim 6; Page 48; 86pp; English.

CC This sequence represents a novel human protein, bcl-w, encoded by the
 CC bcl-2 gene family and extracted from an adult brain library. This gene
 CC promotes cell survival, so its modulation is useful in treatment of
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
 CC ischaemia, human immunodeficiency virus infection or in cell transplants.
 CC Up-regulation of the gene can also be used to modify cell lines cultured
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
 CC and to increase survival of primary explants during genetic modification.
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
 CC antibody production or screening of potential modulators.
 CC Sequence 193 AA;

Query Match 96.0%; Score 1331; DB 1; Length 193;
 Best Local Similarity 93.8%; Pred. No. 2.34e-117;
 Matches 181; Conservative 9; Mismatches 2; Indels 1; Gaps 1;

Db 1 MATPASAPDTRALVADVGVYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETFRRT 60
 QY 1 MPTPASTPTDTRALVADVGVYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETFRRT 60
 Db 61 FSDLAALQHLVTPGSAQQRFTQVSDLEFQGGPNWGRVLAFFLFGAALCAESYNKEMEPLVG 120
 QY 61 FSDLAALQHLVTPGSAQQRFTQVSDLEFQGGPNWGRVLAFFLFGAALCAESYNKEMEPLVG 120
 Db 121 QVQEMWVAYLETRLDVNIHSSGGWAEFTALYGDGAEARLRREGNWSVTVLTGAVAL 180
 QY 121 QVQDMIVAYLETRLDVNIHSSGGWAEFTALYGDGAEARLRREGNWSVTVLTGAVAL 179
 Db 181 GALVTGGAFFASK 193
 QY 180 GALVTGGAFFASK 192

RESULT 11

ID W97394 standard; Protein; 192 AA.
 AC W97394;
 DE 20-MAY-1999 (first entry)
 DE Mammalian bcl-y protein.
 KW Rat bcl-y protein; Bcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite.
 OS Mammalia.
 PN US5883229-A.
 PD 16-MAR-1999.
 PF 25-NOV-1997; 978523.
 PR 23-FEB-1996; US-012201.
 PR 11-FEB-1997; US-798897.
 PR 25-NOV-1997; US-978523.
 PA (COCE-) COCENSYS INC.
 PI Guastella J;
 DR WPI: 99-214150/18.
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
 PT for modulating programmed cell death
 PS Claim 2; Columns 19-22; 26pp; English.
 CC The present sequence represents a mammalian bcl-y protein.
 CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infarction, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis- conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent.
 CC They may also be used in this way to develop cell lines which remain


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SO Sequence 193 AA;
Query Match 96.5%; Score 1337; DB 1; Length 193;
Best Local Similarity 94.3%; Pred. No. 5.93e-118;
Matches 182; Conservative 8; Mismatches 2; Indels 1; Gaps 1;

Db 1 MATPASADPTRALVDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 60
QY 1 MPTPASTPTDTRALVADFGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 60
Db 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFGQGNMGRVAFVFFGAALCAESVKNEMEPLVG 120
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFGQGNMGRVAFVFFGAALCAESVKNEMEPLVG 120
Db 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALEARRLRREGNWSVRTVLTGAVAL 180
QY 121 QVQDMIVAYLETRLADWIHSSGGWADFTALYGDGALEARRLRREGNWA-VSTVVTGAVAL 179
Db 181 GALVTGGAFFASK 193
QY 180 GALVTGGAFFASK 192

RESULT 7
ID W61392 standard; Protein; 193 AA.
AC W61392;
DT 02-OCT-1998 (first entry)
DE Human bcl-2 protein.
KW bcl-2; bcl-2; cell death pathway; apoptotic; apoptosis; human.
OS Homo sapiens.
PN US5789201-A.
PF 04-AUG-1998. 798897.
PR 11-FEB-1997; 798897.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PA (COCE-) COCENSYS INC.
PI Guastella J.
DR N-PSD; 446079/38.
DR N-PSD; 428334.
PT Nucleic acids encoding B-cell lymphoma-2 protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
PS Example; Column 17/18; 27pp; English.
CC The mammalian bcl-2 protein is a member of the bcl-2 family, components
CC in the cell death pathway. The bcl-2 family have both apoptotic activity
CC and the apoptosis blocking activity. bcl-2 falls in the apoptosis
CC activity category. The recombinant protein may be used to prevent
CC uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired.
SQ Sequence 193 AA;

Query Match 96.5%; Score 1337; DB 1; Length 193;
Best Local Similarity 94.3%; Pred. No. 5.93e-118;
Matches 182; Conservative 8; Mismatches 2; Indels 1; Gaps 1;

Db 1 MATPASADPTRALVDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 60
QY 1 MPTPASTPTDTRALVADFGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 60
Db 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFGQGNMGRVAFVFFGAALCAESVKNEMEPLVG 120
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFGQGNMGRVAFVFFGAALCAESVKNEMEPLVG 120
Db 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALEARRLRREGNWSVRTVLTGAVAL 180
QY 121 QVQDMIVAYLETRLADWIHSSGGWADFTALYGDGALEARRLRREGNWA-VSTVVTGAVAL 179
Db 181 GALVTGGAFFASK 193
QY 180 GALVTGGAFFASK 192

RESULT 8
ID W97393 standard; Protein; 192 AA.
AC W97393;
DT 20-MAY-1999 (first entry)
DE protein sequence of the specification.
KW Rat bcl-2 protein; Rbcl-y; human bcl-2 protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite.
OS Unidentified.
PN US583229-A.
PF 16-MAR-1999.
PR 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J.
DR WPI; 99-214150/18.
DT Novel bcl-2 homologues of the rat and human bcl-2 protein - useful
DT for modulating programmed cell death
PS Disclosure; Columns 19-20; 26pp; English.
CC The specification describes rat bcl-2 protein (Rbcl-y) and human bcl-2
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes; head trauma; Alzheimer's Disease; neural and muscular
CC degenerative diseases (especially multiple sclerosis); myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent.
CC They may also be used in this way to develop cell lines which remain
CC viable in culture for an extended period. In contrast, if they act as
CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC conditions associated with prolonged cell life span such as cancer
CC (especially Kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC diseases. They may also be used to cause cell death in, and hence
CC control, parasites.
SQ Sequence 192 AA;

Query Match 96.1%; Score 1332; DB 1; Length 192;
Best Local Similarity 95.3%; Pred. No. 1.86e-117;
Matches 183; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

Db 1 ATPASTPTDTRALVADFGVYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 60
QY 2 PTPASTPTDTRALVADFGVYLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRTF 61
Db 61 SDLAALQHLVTPGSAQQRFTQVSDLELFGQGNMGRVAFVFFGAALCAESVKNEMEPLVGQ 120
QY 62 SDLAALQHLVTPGSAQQRFTQVSDLELFGQGNMGRVAFVFFGAALCAESVKNEMEPLVGQ 121
Db 121 QVQDMIVAYLETRLADWIHSSGGWAEFTALYGDGALEARRLRREGNWSVRTVLTGAVALG 180
QY 122 QVQDMIVAYLETRLADWIHSSGGWADFTALYGDGALEARRLRREGNWA-VSTVVTGAVALG 180
Db 181 ALVTGGAFFASK 192
QY 181 ALVTGGAFFASK 192

RESULT 9
ID Y05532 standard; Protein; 193 AA.
AC Y05532;
DT 05-JUL-1999 (first entry)
DE Human Bcl-w protein essential for spermatogenesis.

```


QY 61 FSDLAQLHVTGSAQQRFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
 Db 121 QVQDWIYVAYLETRLADWIHSSGGWADFTALYGDGALEBARRLREGNWSVTVTGAVALG 180
 QY 121 QVQDWIYVAYLETRLADWIHSSGGWADFTALYGDGALEBARRLREGNWSVTVTGAVALG 180
 Db 181 ALVTVGAFASK 192
 QY 181 ALVTVGAFASK 192

RESULT 2

ID Y05531 standard; Protein; 193 AA.
 AC Y05531
 DT 05-JUL-1999 (first entry)
 DE Mouse Bcl-w protein essential for spermatogenesis.
 KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 KW animal model.
 OS Mus sp.
 PN W09913710-A1.
 PD 25-MAR-1999.
 PF 16-SEP-1998; AU0764.
 PR 16-SEP-1997; AU-009228.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
 DR WPI; 99-243890/20.
 DR N-PSDB; X25133.
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w
 PS Claim 2; Page 35; 52pp; English.
 CC The present sequence is mouse Bcl-w, a pro-survival member of the
 CC Bcl-2 family which is widely expressed and which is essential for
 CC spermatogenesis. The invention relates generally to a method of
 CC treatment and to an animal model for the identification of
 CC molecules and genetic sequences useful for inducing or reducing
 CC fertility of male animals. Methods are provided for the treatment
 CC of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation is at least
 CC one allele of the human or murine bcl-w gene (see X25133-35) or in
 CC a gene associated with bcl-w. Such animals have disorganized
 CC seminiferous tubules and are substantially infertile, but possess no
 CC other major abnormalities as determined by histological examination.
 CC They can be used to screen for therapeutic molecules including
 CC genetic sequences capable of inducing, enhancing or otherwise
 CC facilitating spermatogenesis in animals, or which can induce
 CC infertility.
 CC Sequence 193 AA;

Query Match 97.0%; Score 1345; DB 1; Length 193;
 Best Local Similarity 95.9%; Pred. No. 9.52e-119;
 Matches 185; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

Db 1 MATPASTPTDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
 QY 1 MPTPASTPTDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
 Db 61 FSDLAQLHVTGSAQQRFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
 QY 61 FSDLAQLHVTGSAQQRFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
 Db 121 QVQDWIYVAYLETRLADWIHSSGGWADFTALYGDGALEBARRLREGNWSVTVTGAVAL 180
 QY 121 QVQDWIYVAYLETRLADWIHSSGGWADFTALYGDGALEBARRLREGNWSVTVTGAVAL 180
 Db 181 ALVTVGAFASK 193
 QY 180 GALVTVGAFASK 192

RESULT 3

ID W97391 standard; Protein; 193 AA.
 AC W97391;

DT 20-MAY-1999 (first entry)

DE The rat bcl-y protein.
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
 KW parasite.
 OS Rattus sp.
 PN US5883229-A.
 PD 16-MAR-1999.
 PF 25-NOV-1997; 978523.
 PR 23-FEB-1996; US-012201.
 PR 11-FEB-1997; US-798897.
 PR 25-NOV-1997; US-978523.
 PA (COCE-) COCENSIS INC.
 PI Guastella J;
 DR WPI; 99-214150/18.
 DR N-PSDB; X15945.
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
 PT for modulating programmed cell death
 PS Disclosure; Columns 15-18; 26pp; English.
 CC The present sequence represents rat bcl-y protein (Rbcl-y). The
 CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
 CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
 CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
 CC proteins may be used to treat conditions associated with a disruption of
 CC the cell death pathway. If they act as cell death inhibitors, they may be
 CC used in therapies to treat subjects suffering from: strokes, head trauma,
 CC Alzheimer's Disease, neural and muscular degenerative diseases
 CC (especially multiple sclerosis), myocardial infarction, vitally induced
 CC cell death, aging, spinal cord injuries and amyotrophic lateral
 CC sclerosis- conditions where cells under go premature cell death as a
 CC result of triggers which may or may not be apparent. They may also be
 CC used in this way to develop cell lines which remain viable in culture for
 CC an extended period. In contrast, if they act as cell death stimulators,
 CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
 CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites.
 CC Sequence 193 AA;

Query Match 96.9%; Score 1343; DB 1; Length 193;
 Best Local Similarity 95.3%; Pred. No. 1.50e-118;
 Matches 184; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

Db 1 MATPASTPTDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
 QY 1 MPTPASTPTDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
 Db 61 FSDLAQLHVTGSAQQRFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
 QY 61 FSDLAQLHVTGSAQQRFTQVSDLEFGGPNWGRVAFVFGAALCAESVKNEMEPLVG 120
 Db 121 QVQDWIYVAYLETRLADWIHSSGGWADFTALYGDGALEBARRLREGNWSVTVTGAVAL 180
 QY 121 QVQDWIYVAYLETRLADWIHSSGGWADFTALYGDGALEBARRLREGNWSVTVTGAVAL 180
 Db 181 GALVTVGAFASK 193
 QY 180 GALVTVGAFASK 192

RESULT 4

ID W61391 standard; Protein; 193 AA.
 AC W61391;
 DT 02-OCT-1998 (first entry)
 DE Rat bcl-y protein.
 KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
 OS Rattus sp.
 PN US5789201-A.

(TW)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:17:41 2000; MasPar time 7.56 Seconds
Tabular output not generated. 601.720 Million cell updates/sec

Title: >US-09-155-327B-9
Description: (1-192) from US09155327B.pep
Perfect Score: 1386
Sequence: 1 MPTPASTPDTRALVAFVGV.....VTGVALGALVTVGAFVASK 192

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
1:geneseqp

Statistics: Mean 32.566; Variance 139.419; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
1	1386	100.0	192	1 Y05533	Mouse Bcl-w protein de
2	1345	97.0	193	1 Y05531	Mouse Bcl-w protein es
3	1343	96.9	193	1 W97391	The rat bcl-y protein.
4	1343	96.9	193	1 W61391	Rat bcl-y protein.
5	1341	96.8	193	1 Y05530	Human Bcl-w protein es
6	1337	96.5	193	1 W97392	The human bcl-y protei
7	1337	96.5	193	1 W61392	Human bcl-y protein.
8	1332	96.1	192	1 W97393	Protein sequence of th
9	1331	96.0	193	1 Y05532	Human Bcl-w protein es
10	1331	96.0	193	1 W36047	Human bcl-w protein.
11	1326	95.7	192	1 W97394	Mammalian bcl-y protei
12	1235	89.1	168	1 W36048	Mouse bcl-w protein.
13	1041	75.1	365	1 W59884	Amino acid sequence of
14	623	44.9	225	1 W19396	"Deprenyl" (RTM)-induc
15	623	44.9	233	1 W31530	Human anti-apoptotic B
16	623	44.9	233	1 R68887	Human thymus BCL-XL.
17	623	44.9	233	1 W05821	Bcl-XL protein.
18	556	40.1	239	1 W87810	A human Bcl-2 protein.
19	545	39.3	239	1 W87812	A human Bcl-2-alpha pr
20	545	39.3	239	1 R71404	Human bcl-2 alpha prot
21	545	39.3	239	1 R70331	Human bcl-2 protein.
22	545	39.3	239	1 R42312	Bcl-2 oncogene product
23	545	39.3	239	1 W40217	Human bcl-2.

ALIGNMENTS

RESULT 1
ID Y05533 standard; Protein; 192 AA.

AC Y05533;

DT 05-JUL-1999 (first entry)

DE Mouse Bcl-w protein derivative.

KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;

KW animal model.

OS Mus sp.

PN W09913710-AL.

PD 25-MAR-1999.

PF 16-SEP-1998; AU0764.

PR 16-SEP-1997; AU-009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Adams J, Cory S, Gibson L, Koentgen F, Print C;

DR WPI; 99-243890/20.

DR N-PSDB; X25135.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or

protein associated with Bcl-w

PS Disclosure; Page 39; 52pp; English.

CC The present sequence is described of a derivative of mouse Bcl-w

is widely expressed and which is essential for spermatogenesis.

CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.

CC The invention relates generally to a method of treatment and to an

animal model for the identification of molecules and genetic

sequences useful for inducing or reducing fertility of male animals.

CC Methods are provided for the treatment of infertility, or for

reducing fertility, by modulating spermatogenesis. An animal model

carries a mutation at least one allele of the human or murine

bcl-w gene (see X25132-35) or in a gene associated with bcl-w.

CC Such animals have disorganised seminiferous tubules and are

substantially infertile, but possess no other major abnormalities

as determined by histological examination. They can be used to

screen for therapeutic molecules including genetic sequences

capable of inducing, enhancing or otherwise facilitating

spermatogenesis in animals, or which can induce infertility.

SQ Sequence 192 AA;

Query Match 100.0%; Score 1386; DB 1; Length 192;

Best Local Similarity 100.0%; Pred. No. 8.04e-123;

Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MPTPASTPDTRALVAFVGVRLQKGVCCGCGECPADPLHQAMRAAGDEFETFRRT 60

QY 1 MPTPASTPDTRALVAFVGVRLQKGVCCGCGECPADPLHQAMRAAGDEFETFRRT 60

Db 61 FSDLAALHVTGSAQORFTQVDELFGQGNWGRVAFVFGAALCAESVKNMEPLVG 120

RA HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
RL Int. Immunol. 0:0-0(1998).
DR EMBL: U23781; AAB97956.1; -.
DR EMBL: U23780; AAB97956.1; JOINED.
DR MGD: MGI:1278325; Bcl2ald.
DR PROSITE: PS01080; BH1; 1.
DR PFAM: PF00452; Bcl-2; 1.
SQ SEQUENCE 172 AA; 20048 MW; 1B340DDD CRC32;

Query Match 11.6%; Score 162; DB 11; Length 172;
Best Local Similarity 32.6%; Pred. No. 8.16e-11;
Matches 28; Conservative 20; Mismatches 31; Indels 7; Gaps 5;
Db 58 DFHVESIDTARIENOVMEKEFEFGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
QY 67 QLVHTP-GSAQRTQVSDLEFGGP-NWGRLVAFFLFGALCAESYNKEMEPL-VG--- 120
Db 117 QVSSFVAEFIMNNTGEWIRNGWED 142
QY 121 QVQEMWVAYLETRLDVTHSSGNAE 146

RESULT 13
ID Q9W6F1 PRELIMINARY; PRT; 211 AA.
AC Q9W6F1;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE MYELOID CELL LEUKEMIA PROTEIN MCL-1 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 99190706.
RA LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.;
RT "Role of Nr13 in regulation of programmed cell death in the bursa of
RT Fabricius".
RL Genes Dev. 13:718-728(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA SOFER L., BURNSIDE J.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF120210; AAD31644.1; -.
DR PROSITE: PS01080; BH1; 1.
FT NON_TER 1
SQ SEQUENCE 211 AA; 23143 MW; DEE4E997 CRC32;

Query Match 11.2%; Score 156; DB 13; Length 211;
Best Local Similarity 22.0%; Pred. No. 8.69e-10;
Matches 29; Conservative 32; Mismatches 70; Indels 1; Gaps 1;
Db 55 PGRASSAVMEKALETLRRVGGVQKHELAFQGLRKLKLEKDDLOAVCEVAQVFNDDG 114
QY 31 AGPGGPAADPLHQMAAGDEFETRFRRTFSDLAALHVTTPGSAQORFTQVSDLEFGG 90
Db 115 VTWNGRVVTLISGAFVAKHLKLSINQEKITSLAGITDALVSKRWLMSQGGWEGFYD 174
QY 91 -PNWGRLVAFFLFGALCAESYNKEMEPLVGQVQEMWVAYLETRLDVTHSSGNAEFTA 149
Db 175 FFRVEDLESSIR 186
QY 150 LYDGALEEAR 161

RESULT 14
ID O77738 PRELIMINARY; PRT; 80 AA.
AC O77738;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE BAK PROTEIN (FRAGMENT).

GN BAK.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RA BARTLING B., HOFFMANN J., HOLTZ J., SCHULZ R., HEUSCH G., DARMER D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig".
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ001204; CAA04598.1; -.
DR HSSP: Q16611; 1BXL.
DR PROSITE: PS01259; BH3; 1.
DR PFAM: PF00452; Bcl-2; 1.
KW Apoptosis.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 8818 MW; 973BE2D0 CRC32;

Query Match 10.3%; Score 144; DB 6; Length 80;
Best Local Similarity 35.4%; Pred. No. 8.91e-08;
Matches 17; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
Db 33 GDDINRRYDSEFQAMLQHLQPTAENAYEFTKIASLFSFGINWGRV 80
QY 50 GDEFETRFRRTFSDLAALHVTTPGSAQORFTQVSDLEFGGPNWGLV 97

RESULT 15
ID Q9Y3R2 PRELIMINARY; PRT; 923 AA.
AC Q9Y3R2;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE NUCLEAR TRANSPORT RECEPTOR.
GN MTR10A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA KUTAY U., IZAURRALDE E., HARTMANN E., GOERLICH D.;
RT "A human homologue of yeast Mtr10p and its role in nuclear protein
RT import".
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ133769; CAB2643.1; -.
KW Receptor.
SQ SEQUENCE 923 AA; 104203 MW; 1661174C CRC32;

Query Match 8.5%; Score 119; DB 4; Length 923;
Best Local Similarity 32.9%; Pred. No. 8.14e-04;
Matches 28; Conservative 15; Mismatches 39; Indels 3; Gaps 3;
Db 383 EPDHGVPEETDDFGE-FRMVRSDLVKDLIFLIGSME-CFAQLYSTLKEGPPWF-VTEA 439
QY 40 DPLHQMAAGDEFETRFRRTFSDLAALHVTTPGSAQORFTQVSDLEFGGPNWGLVAF 99
Db 440 VLFMAATAKSDVPNNPLVEVLE 464
QY 100 FLFGALCAESYNKEMEPLVGQVQE 124

Search completed: Fri Jun 23 14:15:48 2000
Job time : 36 secs.

DATE RECEIVED 10/27/71

KC
STATINT-LEJ/JVA, 110000E T000Z JAN 76

UNCLAS


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QY 181 GALVTVGGAFFASK 193
RESULT 2
ID O35844 PRELIMINARY; PRT; 233 AA.
AC O35844;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE BCL2-LIKE (BCL-XL).
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B6/CBA; TISSUE-THYMUS;
RX MEDLINE; 98051053.
RA "A novel Bcl-x isoform connected to the T cell receptor regulates
RT apoptosis in T cells."
RL Immunity 7:629-639(1997).
DR EMBL; U51278; AAC53459.1; -.
DR HSSP; P53563; 1AF3.
DR MGD; MGI:88139; Bcl2L.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PFAM; PF00452; Bcl-2; 1.
SQ SEQUENCE 233 AA; 26033 MW; A4A14278 CRC32;

Query Match 45.1%; Score 630; DB 11; Length 233;
Best Local Similarity 53.8%; Pred. No. 1.97e-106; Indels 2; Gaps 2;
Matches 78; Conservative 30; Mismatches 35;

Db 85 AVKQALREAGDEFELRYRAFSDLTSQLHITPGTAYQSFQVNVNLFDRDGYNNGRIVAF 144
QY 41 PLHQAMRAAGDEFETFRRTFSDLAQLHVTTPGSAQORFTQVSDQLFGQGNWGLVAF 100
Db 145 SFGGALCVESVDKEMQVLSRIASNMATYLNHLEPWIQENGWDTFVLDYGNNAE 204
QY 101 LFGAALCAESVKNEMEPVGVQVEMVAYLETRLVDMTHSSGGWAEFTALYGDGAL 160
Db 205 KGKGFNEWLTGTWAGVLLGSL 229
QY 161 LRUEG-N-WASVRTVLTGAVALGAL 183

RESULT 3
ID O02718 PRELIMINARY; PRT; 229 AA.
AC O02718;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE BCL-2 (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN; TISSUE-THYMUS;
RA REYES R.A.; COCKERELL G.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92434; AAB53319.1; -.
DR HSSP; P53563; 1AF3.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PFAM; PF00452; Bcl-2; 1.
FT NON_TER 229

SQ SEQUENCE 229 AA; 25099 MW; E82B3DFB CRC32;

Query Match 42.2%; Score 590; DB 6; Length 229;
Best Local Similarity 44.5%; Pred. No. 9.22e-98; Indels 5; Gaps 3;
Matches 73; Conservative 46; Mismatches 40;

Db 71 AAGPAPSPVPVVTLTROAGDDFRRYRRDFAEMSSQLHLTPFTAREFRATVVEELFRD 130
QY 30 GAGCGEPAADPLHQAMRAAGDEFETFRRTFSDLAQLHVTTPGSAQORFTQVSDQLFG 89
Db 131 GYNWGRIVAFPEFGVCMVESVNRNEMSLVDLSIALWMTYLNHLEPWIQENGWDAFVE 190
QY 90 GPNWGRIVAFPEFGVCMVESVNRNEMSLVDLSIALWMTYLNHLEPWIQENGWDAFVE 149
Db 191 LYGP-SM---RPLDFSWLSLKLALLSLAL-VGACITLGLAYLGHK 229
QY 150 LYGDGALAEARRLRUEGNWASVRTVLTGAVALGALVTVGGAFFASK 193

RESULT 4
ID O35843 PRELIMINARY; PRT; 235 AA.
AC O35843;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE BCL2-LIKE (BCL-X-GAMMA).
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B6/CBA; TISSUE-THYMUS;
RX MEDLINE; 98051053.
RA "A novel Bcl-x isoform connected to the T cell receptor regulates
RT apoptosis in T cells."
RL Immunity 7:629-639(1997).
DR EMBL; U51277; AAC53458.1; -.
DR HSSP; P53563; 1AF3.
DR MGD; MGI:88139; Bcl2L.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PFAM; PF00452; Bcl-2; 1.
SQ SEQUENCE 235 AA; 26122 MW; FB0B0207 CRC32;

Query Match 38.3%; Score 535; DB 11; Length 235;
Best Local Similarity 59.0%; Pred. No. 6.46e-86; Indels 0; Gaps 0;
Matches 62; Conservative 24; Mismatches 19;

Db 85 AVKQALREAGDEFELRYRAFSDLTSQLHITPGTAYQSFQVNVNLFDRDGYNNGRIVAF 144
QY 41 PLHQAMRAAGDEFETFRRTFSDLAQLHVTTPGSAQORFTQVSDQLFGQGNWGLVAF 100
Db 145 SFGGALCVESVDKEMQVLSRIASNMATYLNHLEPWIQENGW 189
QY 101 LFGAALCAESVKNEMEPVGVQVEMVAYLETRLVDMTHSSGGWA 145

RESULT 5
ID Q9WUI5 PRELIMINARY; PRT; 170 AA.
AC Q9WUI5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE BCL-X SHORT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;

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WIRE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Jun 23 14:15:12 2000; MasPar time 18.46 Seconds
Tabular output not generated. 724.726 Million cell updates/sec

Title: >US-09-155-327B-7
Description: (1-193) from US09155327B.pep
Perfect Score: 1397
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFASK 193

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 44.702; Variance 83.297; scale 0.537

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1378	98.6	193	11	BCL-W.	5.72e-273
2	630	45.1	233	11	BCL2-LIKE (BCL-XL).	1.97e-106
3	590	42.2	229	6	BCL-2 (FRAGMENT).	9.22e-98
4	535	38.3	235	11	BCL2-LIKE (BCL-X-GAMMA	6.46e-86
5	207	14.8	170	11	BCL-X SHORT.	6.91e-19
6	175	12.5	213	11	BCL-2-RELATED OVARIAN	4.38e-13
7	170	12.2	174	13	PROTEIN A1.	3.32e-12
8	169	12.1	170	11	BCL-2-RELATED OVARIAN	4.97e-12
9	167	12.0	331	11	EAT/MCL-1 PROTEIN (MCL	1.11e-11
10	165	11.8	330	11	MCL-1 PROTEIN.	2.47e-11
11	163	11.7	172	11	B-CELL LEUKEMIA/LYMPHO	5.48e-11
12	162	11.6	172	11	B-CELL LEUKEMIA/LYMPHO	8.16e-11
13	156	11.2	211	13	MYELOID CELL LEUKEMIA	8.69e-10
14	144	10.3	80	6	BAK PROTEIN (FRAGMENT)	8.91e-08
15	119	8.5	923	4	NUCLEAR TRANSPORT RECE	8.14e-04
16	117	8.4	128	11	B-CELL LEUKEMIA/LYMPHO	1.63e-03
17	103	7.4	1259	5	C42C1.4 PROTEIN.	1.72e-01
18	102	7.3	451	2	HYPOTHETICAL 46.4 KD P	2.36e-01
19	100	7.2	975	4	TRANSPORTIN-SR.	2.36e-01
20	100	7.2	168	14	SIMILAR TO BCL-FAMILY	4.44e-01

21	101	7.2	378	2	O53318	HYPOTHETICAL 42.6 KD P	3.24e-01
22	100	7.2	440	1	O9YFI3	440AA LONG HYPOTHETICA	4.44e-01
23	100	7.2	451	5	P90814	F46C5.9 PROTEIN.	4.44e-01
24	100	7.2	505	1	O27209	CONSERVED PROTEIN (FLP	4.44e-01
25	100	7.2	505	1	O50517	HYPOTHETICAL 55.1 KD P	4.44e-01
26	99	7.1	967	5	Q18965	D2013.5 PROTEIN.	6.07e-01
27	98	7.0	521	14	O9YTU1	GAG PROTEIN.	8.28e-01
28	98	7.0	572	5	O19345	NHR-25 PROTEIN.	8.28e-01
29	98	7.0	579	14	Q65605	SURFACE ENVELOPE PROTE	8.28e-01
30	96	6.9	757	14	O37361	PUTATIVE RNA DEPENDENT	1.53e+00
31	95	6.8	130	14	P87527	SURFACE ENVELOPE PROTE	2.07e+00
32	95	6.8	148	14	P87532	SURFACE ENVELOPE PROTE	2.07e+00
33	95	6.8	148	14	P87531	SURFACE ENVELOPE PROTE	2.07e+00
34	95	6.8	256	2	O92657	MORPHINE 6-DEHYDROGENA	2.07e+00
35	95	6.8	597	14	O9YUR4	TERMINAL PROTEIN.	2.07e+00
36	95	6.8	630	5	Q24222	METALLOPEPTIDASE.	2.07e+00
37	95	6.8	668	2	Q51711	CYTCHROME BA (EC 1.9.	2.07e+00
38	95	6.8	1053	2	P77865	ENDOGLUCANASE F PRECUR	2.07e+00
39	93	6.7	130	14	P87529	SURFACE ENVELOPE PROTE	3.78e+00
40	93	6.7	131	14	P90358	SURFACE ENVELOPE PROTE	3.78e+00
41	94	6.7	279	14	O57148	SEROTYPE B PUTATIVE MA	2.80e+00
42	93	6.7	576	14	Q65604	SURFACE ENVELOPE PROTE	3.78e+00
43	94	6.7	585	14	Q65603	SURFACE ENVELOPE PROTE	2.80e+00
44	94	6.7	896	1	O30061	MOLYBDOPTERIN OXIDORED	2.80e+00
45	93	6.7	1937	2	O30482	PKS MODULE 4.	3.78e+00

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	193 AA.
AC	O88996;			
DT	01-NOV-1998 (TREMBlrel. 08, Created)			
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)			
DT	01-NOV-1999 (TREMBlrel. 12, Last annotation update)			
DE	BCL-W.			
GN	BCL-W.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eucheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;			
RA	HAMNER S., SKOGLOSA Y., LINDHOLM D.;			
RT	"Differential expression of Bcl-w and Bcl-x mRNA in the developing and			
RT	adult nervous system.";			
RL	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF096291; AAC64200.1; -.			
DR	HSSP; P53563; 1AF3.			
DR	PROSITE; PS01080; BH1; 1.			
DR	PROSITE; PS01258; BH2; 1.			
DR	PROSITE; PS01260; BH4_1; 1.			
DR	PFAM; PF00452; Bcl-2; 1.			
SQ	SEQUENCE 193 AA; 20820 MW; 6E5F84BA CRC32;			

Query Match		98.6%	Score 1378;	DB 11;	Length 193;
Best Local Similarity		97.4%	Pred. No. 5.72e-273;		
Matches 188;		Conservative 4;	Mismatches 1;	Indels 0;	Gaps 0;
Db	1	MATPASTPDTRALVADFVGYKLRQYKVGAGPGCGPAGDPLHQAMRAAGDEFTFRRT	60		
Qy	1	MATPASAPDTRALVADFVGYKLRQYKVGAGPGCGPAGDPLHQAMRAAGDEFTFRRT	60		
Db	61	FSDLAALHVTGSAQORFTQVSDLEFGQGNWGRVAVFFVFGAALCAESVKNMEPLVG	120		
Qy	61	FSDLAALHVTGSAQORFTQVSDLEFGQGNWGRVAVFFVFGAALCAESVKNMEPLVG	120		
Db	121	QVQDWMTYLETRLADNTHSSGGWAEFTALYDGCALREARLRGNWASVTVLTGVAL	180		
Qy	121	QVQDWMTYLETRLADNTHSSGGWAEFTALYDGCALREARLRGNWASVTVLTGVAL	180		
Db	181	GALVTVGAFASK 193			
Qy	181	GALVTVGAFASK 193			

Search completed: Fri Jun 23 14:14:23 2000
Job time : 20 secs.

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RESULT 14
ENTRY      D37332      #type complete
TITLE      transforming protein (bcl-2-beta) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
          23-Feb-1997
ACCESSIONS D37332
REFERENCE   A37332
#authors   Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal   Nucleic Acids Res. (1992) 20:4187-4192
#title     Isolation and characterization of the chicken bcl-2 gene:
          expression in a variety of tissues including lymphoid and
          neuronal organs in adult and embryo.
#cross-references MUID:92375724
#accession D37332
#status    preliminary; nucleic acid sequence not shown; not
          compared with conceptual translation
          ##molecule_type DNA
          ##residues 1-206 ##label EGU
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS      mitochondrion
SUMMARY       #length 206 #molecular-weight 22440 #checksum 5581

Query Match 36.6%; Score 511; DB 2; Length 206;
Best Local Similarity 49.6%; Pred. No. 1.33e-76;
Matches 57; Conservative 29; Mismatches 29; Indels 0; Gaps 0;

Db 82 AAGPALSPVPVHLTLRQAGDDFSRRYRDRFAEMSSQLHLTPFTARGRFATVVEELFRD 141
   :|||: : : : :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Qy 30 GAGPGEGPAADPLHQAMRAAGDEFETFRRTFSDLAQLHLVTPGSAQQRFTQVSDLELF 89
   :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 142 GVNWGRIVAFEFEGVGVNREMSPLVDNIALMTTEYLNRHLHTWIQDNGGW 196
   :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Qy 90 GPNWRLVAFLLFGALCAESVKNEMEPLVGQVQEWVAYLETRLDVNIHSSGGW 144

RESULT 15
ENTRY      TVMSB1      #type complete
TITLE      transforming protein bcl-2-beta - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
          18-Jun-1999
ACCESSIONS B25960
REFERENCE   A90893
#authors   Negrini, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
          C.M.
#journal   Cell (1987) 49:455-463
#title     Molecular analysis of mbcl-2: structure and expression of the
          murine gene homologous to the human gene involved in
          follicular lymphoma.
#cross-references MUID:87187643
#accession B25960
          ##molecule_type DNA
          ##residues 1-199 ##label NEG
#cross-references GB:M16506; NID:9468335; PIDN:AAA37281.1; PID:g387110
GENETICS
#gene      BCL2
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS      alternative splicing; transforming protein
SUMMARY       #length 199 #molecular-weight 22299 #checksum 7397

Query Match 36.4%; Score 509; DB 1; Length 199;
Best Local Similarity 49.6%; Pred. No. 3.39e-76;
Matches 58; Conservative 28; Mismatches 31; Indels 0; Gaps 0;

Db 76 VATAGPALSPVPPCVHLTLRAGDDFSRRYRDRFAEMSSQLHLTPFTARGRFATVVEELF 135
   :|||: : : : :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Qy 28 VCGAGPGEGPAADPLHQAMRAAGDEFETFRRTFSDLAQLHLVTPGSAQQRFTQVSDLELF 87
   :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 136 RDGVNWRIVAFEFEGVGVNREMSPLVDNIALMTTEYLNRHLHTWIQDNGGW 192
   :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Qy 88 QGGPNWRLVAFLLFGALCAESVKNEMEPLVGQVQEWVAYLETRLDVNIHSSGGW 144
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#title Molecular cloning and DNA sequence analysis of cDNA encoding
#cross-references MUID:92379084
#accession S24390
#status preliminary
#molecule_type mRNA
#residues 1-232 #label CAZ
#cross-references EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS mitochondrion; transmembrane protein
SUMMARY #length 232 #molecule-weight 25839 #checksum 1516

Query Match 40.6%; Score 567; DB 2; Length 232;
Best Local Similarity 46.5%; Pred. No. 5.16e-88;
Matches 74; Conservative 38; Mismatches 41; Indels 6; Gaps 4;

Db 79 GCAAPGCVHIALRQAGDEFRRYORPQMSGQLHTPTATGRFVAVVEELFRDGVNWW 138
QY 36 GPAADP-LHQAMRAAGDEFRRFTFSDLAQLHVTGPSAQQRFTQVSDLELFGQGNNG 94

Db 139 RIVAFPEFGVMCVESVYNRMSPLVNIAITWMTXYLNRLHNWIODNGWDVAFVLYGN- 197
QY 95 RLVAFFLFGAALCAESVKNKMEPLVGQVQWVMVAYLETRLVDWIHSSGGWAEFTALYD 154

Db 198 SM---RPLDFSWISLTKTILS-LVLVGACITTLGAYLGHK 232
QY 155 ALEEARLRGNASVRTVLTGAVALGALVTYGAFFASK 193

RESULT 11
ENTRY bcl-x transmembrane deleted - mouse
TITLE #formal_name Mus musculus #common_name house mouse
ORGANISM 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
DATE 16-Jul-1999

ACCESSIONS I49057
REFERENCE I49057
#authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in B
#cross-references MUID:95052604
#accession I49057
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-214 #label RES
#cross-references EMBL:U010102; NID:g506649; PIDN:AAA82174.1;
PID:g506650

GENETICS
#gene bcl-x-long
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY #length 214 #molecule-weight 23900 #checksum 9730

Query Match 38.9%; Score 543; DB 2; Length 214;
Best Local Similarity 58.9%; Pred. No. 4.13e-83;
Matches 63; Conservative 23; Mismatches 21; Indels 0; Gaps 0;

Db 85 AVKQALREAGDEFLRYRAFSDLTSQHLITPGTAYQSFQVNVNELFRDGVNWGRIVAF 144
QY 41 PLHQAMRAAGDEFRRFTFSDLAQLHVTGPSAQQRFTQVSDLELFGQGNWRLVAF 100

Db 145 SFGGALCVESVDKEMQVLVSRTASMTATYLNHLEPWIQENGWGTFF 191
QY 101 LFGAALCAESVKNKMEPLVGQVQWVMVAYLETRLVDWIHSSGGWAEF 147

RESULT 12
ENTRY JE0203
TITLE apoptosis regulator bcl-x isoform - human
ALTERNATE_NAMES h-bcl-xbeta
ORGANISM #formal_name Homo sapiens #common_name man
DATE 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
16-Jul-1999
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ACCESSIONS JE0203
REFERENCE JE0203
#authors Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler,
E.
#journal Biochem. Biophys. Res. Commun. (1998) 248:147-152
#title Identification of a human cDNA encoding a novel bcl-x
isoform.
#cross-references MUID:98340865
#accession JE0203
#molecule_type mRNA
#residues 1-227 #label BAN
#cross-references GB:U72398; NID:g1622940; PIDN:AAB17354.1;
PID:g1622941

GENETICS
#gene bcl-x
#map_position 20
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY #length 227 #molecule-weight 25290 #checksum 864

Query Match 38.5%; Score 538; DB 2; Length 227;
Best Local Similarity 53.7%; Pred. No. 4.32e-82;
Matches 65; Conservative 27; Mismatches 29; Indels 0; Gaps 0;

Db 85 AVKQALREAGDEFLRYRAFSDLTSQHLITPGTAYQSFQVNVNELFRDGVNWGRIVAF 144
QY 41 PLHQAMRAAGDEFRRFTFSDLAQLHVTGPSAQQRFTQVSDLELFGQGNWRLVAF 100

Db 145 SFGGALCVESVDKEMQVLVSRTASMTATYLNHLEPWIQENGWGTFF 204
QY 101 LFGAALCAESVKNKMEPLVGQVQWVMVAYLETRLVDWIHSSGGWAEFTALYD 160

Db 205 R 205
QY 161 R 161

RESULT 13
ENTRY A47537 #type complete
TITLE apoptosis regulator bcl-x - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change
16-Jul-1999

ACCESSIONS A47537
REFERENCE A47537
#authors Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
Lindsten, T.; Furka, L.A.; Mao, X.; Nunez, G.; Thompson,
C.B.
#journal Cell (1993) 74:597-608
#title bcl-x, a bcl-2-related gene that functions as a dominant
regulator of apoptotic cell death.
#cross-references MUID:93364977
#accession A47537
#status preliminary
#molecule_type DNA
#residues 1-190 #label BOI
#cross-references GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1;
PID:g510899

CLASSIFICATION #superfamily bcl transforming protein
SUMMARY #length 190 #molecule-weight 21467 #checksum 5509

Query Match 38.4%; Score 537; DB 2; Length 190;
Best Local Similarity 59.8%; Pred. No. 6.90e-82;
Matches 67; Conservative 20; Mismatches 24; Indels 1; Gaps 1;

Db 79 ASDVRQALRDAGDEFLRYRAFSDLTSQHLITPGTAYQSFQVNVNELFRDGVNWGRIV 138
QY 39 ADPLHQAMRAAGDEFRRFTFSDLAQLHVTGPSAQQRFTQVSDLELFGQGNWRLVAF 98

Db 139 FFSFGGALCVESVDKEMQVLVSRTASMTATYLNHLEPWIQENGWGTFF-TAL 189
QY 99 FFLFGAALCAESVKNKMEPLVGQVQWVMVAYLETRLVDWIHSSGGWAEFTAL 150
16-Jul-1999
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ORGANISM      #formal_name Rattus norvegicus #common_name Norway rat
DATE          29-May-1998 #sequence_revision 29-May-1998 #text_change
ACCESSIONS    I53744
REFERENCE      Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
#journal      Gene (1994) 140:291-292
#title        Cloning and sequencing of a cDNA encoding the rat Bcl-2
#cross-references MUID:94193015
#accession    I53744
#status       preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues     1-236 #label RES
#cross-references GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
GENETICS
#gene         bcl-2
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY       #length 236 #molecular-weight 26550 #checksum 8001
Query Match  41.4%; Score 579; DB 2; Length 236;
Best Local Similarity 44.6%; Pred. No. 1.80e-90;
Matches 74; Conservative 43; Mismatches 44; Indels 5; Gaps 3;
Db 76 VANAGPALSPPVPHVLTLLRAGDDFRYYRRDFAEMSSQLHLPPTARGRFATVVEELF 135
QY 28 VCGAGGEGPADPLHQAMRAAGDEFETFRFTFSDLAALHVTGPSAQQRFTQVSDELF 87
Db 136 RDGVNMGRIYAFFEFGVCMVSVNREMSPLVDNIALWTEYLNRHLHTWIQDNGWDAF 195
QY 88 QGGPNMGRVLAFFLFGAALCAESVKNEMEPVGVQVEMVAYLETRLVDMTHSSGGWAEF 147
Db 196 VELYGP-SM---RPLDFSWLSLTLTLAL-VGACITLGLYGHK 236
QY 148 TALYGDGALEEARLRREGNWSVTRVLTGVALGALVTVGAFASK 193
RESULT 8
ENTRY    167431 #type complete
TITLE    BCL-X-Long - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE     26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS 167431
REFERENCE  Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
#authors   Endocrinology (1995) 136:232-241
#journal   Expression of members of the bcl-2 gene family in the
#title     immature rat ovary: equine chorionic gonadotropin-mediated
           inhibition of granulosa cell apoptosis is associated with
           decreased bax and constitutive bcl-2 and bcl-xlong
           messenger ribonucleic acid levels.
#cross-references MUID:95129487
#accession 167431
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-233 #label RES
#cross-references EMBL:U34963; NID:g1004376; PIDN:AAA77686.1;
           PID:g1004377
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY       #length 233 #molecular-weight 26122 #checksum 8310
Query Match  41.3%; Score 577; DB 2; Length 233;
Best Local Similarity 50.3%; Pred. No. 4.62e-90;
Matches 73; Conservative 31; Mismatches 39; Indels 2; Gaps 2;
Db 85 AVKQALREAGDEFELRYRAFSDLTFSQLHTPTGTYQVFEQVYNELFRDGVNMGRIYASS 144
QY 41 PLHQAMRAAGDEFETFRFTFSDLAALHVTGPSAQQRFTQVSDELFQGGPNMGRVLAFF 100
Db 145 SFGGALCVESVDKEMQVLVSRISATSWATYLNHLEPWIQENGWDTFFVDLYGNNTAPESR 204
QY 101 LFGAALCAESVKNEMEPVGVQVEMVAYLETRLVDMTHSSGGWAEFTALYGDGALEEAR 160
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Db 205 KGQERENRWFVTGMTVAGVVLGSL 229
QY 161 RLREG-N-WASVRTVLTGVALGAL 183
RESULT 9
ENTRY    TVMSAL #type complete
TITLE    transforming protein bcl-2-alpha - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
ACCESSIONS A25960; E37332
REFERENCE  Negri, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
#journal   Cell (1987) 49:455-463
#title     Molecular analysis of mbcl-2: structure and expression of the
           murine gene homologous to the human gene involved in
           follicular lymphoma.
#cross-references MUID:87187643
#accession A25960
#molecule_type DNA
#residues  1-236 #label NEG
#cross-references GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1;
           PID:g387109
REFERENCE A37332
#authors   Euchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal   Nucleic Acids Res. (1992) 20:4187-4192
#title     Isolation and characterization of the chicken bcl-2 gene:
           expression in a variety of tissues including lymphoid and
           neuronal organs in adult and embryo.
#cross-references MUID:92375724
#accession E37332
#status     preliminary; nucleic acid sequence not shown; not
           compared with conceptual translation
#molecule_type DNA
#residues  1-33, 'E', 34-220, 'AL', 223-236 #label EGU
GENETICS
#gene      BCL2
#introns   192/3
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS      alternative splicing; mitochondrion; transforming protein;
           transmembrane protein
SUMMARY       #length 236 #molecular-weight 26524 #checksum 6709
Query Match  40.9%; Score 572; DB 1; Length 236;
Best Local Similarity 44.6%; Pred. No. 4.89e-89;
Matches 74; Conservative 43; Mismatches 44; Indels 5; Gaps 3;
Db 76 VATAGPALSPPVPCVHLTLRAGDDFRYYRRDFAEMSSQLHLPPTARGRFATVVEELF 135
QY 28 VCGAGGEGPADPLHQAMRAAGDEFETFRFTFSDLAALHVTGPSAQQRFTQVSDELF 87
Db 136 RDGVNMGRIYAFFEFGVCMVSVNREMSPLVDNIALWTEYLNRHLHTWIQDNGWDAF 195
QY 88 QGGPNMGRVLAFFLFGAALCAESVKNEMEPVGVQVEMVAYLETRLVDMTHSSGGWAEF 147
Db 196 VELYGP-SM---RPLDFSWLSLTLTLAL-VGACITLGLYGHK 236
QY 148 TALYGDGALEEARLRREGNWSVTRVLTGVALGALVTVGAFASK 193
RESULT 10
ENTRY    S24390 #type complete
TITLE    transforming protein (Bcl-2) homolog - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE     13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
ACCESSIONS S24390
REFERENCE  Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
#authors   Biochim. Biophys. Acta (1992) 1132:109-113
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QY 41 PLHQAMRAAGDEFEFRTRFTSDLAALQHLVTPGSAQORFTQVSDELFQGGPNWRLVAF 100
Db 145 SFGGALCVESVDKEMQVLVSRIASWATYLNHLEPWIQENGWDTFVLYGNNAAESR 204
QY 101 LFGAALCAESVKNEMEPVGVQVEMVAYLETRLDVHISSGGWAEFTALYGDGALEEAR 160
Db 205 KQGRFNRFWLTGMTVAGVLLGSL 229
QY 161 RLREG-N-WASVRTVLTGAVALGAL 183

RESULT 2
ENTRY 2
TITLE BCL-X protein - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999
ACCESSIONS S51761; S51762
REFERENCE S51761
#authors Michaelidis, T.M.
#submission submitted to the EMBL Data Library, November 1994
#accession S51761
#status preliminary
#molecule_type DNA
#residues 1-233 #label MIC
#cross-references EMBL:X82537; NID:g607176; PIDN:CAA57886.1;
PID:g607177

REFERENCE S51761
#authors Michaelidis, T.M.
#submission submitted to the EMBL Data Library, November 1994
#accession S51762
#status preliminary
#molecule_type DNA
#residues 1-125,189-233 #label MIC
#cross-references EMBL:X82537; NID:g607176; PIDN:CAA57887.1;
PID:g607178

GENETICS 125/3
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CLASSIFICATION #superfamily bcl transforming protein
SUMMARY #length 233 #molecular-weight 26130 #checksum 6378

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Best Local Similarity 53.1%; Pred. No. 7.19e-98;
Matches 77; Conservative 30; Mismatches 36; Indels 2; Gaps 2;

Db 85 AVKQALREAGDEFELRYRAFSDLTSQHLITPGTAYQSFQVNVNLFDRDGVNWGRIVAF 144
QY 41 PLHQAMRAAGDEFEFRTRFTSDLAALQHLVTPGSAQORFTQVSDELFQGGPNWRLVAF 100
Db 145 SFGGALCVESVDKEMQVLVSRIASWATYLNHLEPWIQENGWDTFVLYGNNAAESR 204
QY 101 LFGAALCAESVKNEMEPVGVQVEMVAYLETRLDVHISSGGWAEFTALYGDGALEEAR 160
Db 205 KQGRFNRFWLTGMTVAGVLLGSL 229
QY 161 RLREG-N-WASVRTVLTGAVALGAL 183

RESULT 3
ENTRY 3
TITLE bcl-x long - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
ACCESSIONS I49056; S52866
REFERENCE I49056
#authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in B
and T lymphocytes.
#cross-references MUID:95052604
#accession I49056
#status preliminary; translated from GB/EMBL/DBJ

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#molecule_type mRNA
#residues 1-233 #label RES
#cross-references EMBL:U10101; NID:g506647; PIDN:AAA82173.1;
PID:g506648
REFERENCE S52866
#authors Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
#submission submitted to the EMBL Data Library, November 1994
#description IL-5 inhibits anti-IGM-induced apoptosis in an immature B
cell line through induction of bcl-XL.
#accession S52866
#status preliminary
#molecule_type mRNA
#residues 1-233 #label KAM
#cross-references EMBL:X83574; NID:g695622; PIDN:CAA58557.1;
PID:g695623
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY #length 233 #molecular-weight 26132 #checksum 5739

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Matches 77; Conservative 30; Mismatches 36; Indels 2; Gaps 2;

Db 85 AVKQALREAGDEFELRYRAFSDLTSQHLITPGTAYQSFQVNVNLFDRDGVNWGRIVAF 144
QY 41 PLHQAMRAAGDEFEFRTRFTSDLAALQHLVTPGSAQORFTQVSDELFQGGPNWRLVAF 100
Db 145 SFGGALCVESVDKEMQVLVSRIASWATYLNHLEPWIQENGWDTFVLYGNNAAESR 204
QY 101 LFGAALCAESVKNEMEPVGVQVEMVAYLETRLDVHISSGGWAEFTALYGDGALEEAR 160
Db 205 KQGRFNRFWLTGMTVAGVLLGSL 229
QY 161 RLREG-N-WASVRTVLTGAVALGAL 183

RESULT 4
ENTRY 4
TITLE transforming protein (bcl-2-alpha) - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
ACCESSIONS A37332; S35453
REFERENCE A37332
#authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neutonal organs in adult and embryo.
#cross-references MUID:92375724
#accession A37332
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-233 #label EGU
#cross-references EMBL:D11381

GENETICS 189/3
#introns
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS mitochondrion; transforming protein; transmembrane protein
SUMMARY #length 233 #molecular-weight 25687 #checksum 99

Query Match 42.0%; Score 587; DB 2; Length 233;
Best Local Similarity 46.6%; Pred. No. 4.11e-92;
Matches 76; Conservative 41; Mismatches 39; Indels 7; Gaps 5;

Db 76 PAEGLRAPPVGVHLALRQAGDEFRRYQDRDFAQMSGLHLTPFTHAGRFVAVVEELFRDG 135
QY 33 PGGG-PAADP-LHQAMRAAGDEFEFRTRFTSDLAALQHLVTPGSAQORFTQVSDELFQGG 90
Db 136 VNWGRIVAFEFQGVCMVSVNREMPLVDNIATWTATYELNRLHNLHIWIODGWDFAVEL 195
QY 91 PNWGRVAFELFGLAALCAESVKNEMEPVGVQVEMVAYLETRLDVHISSGGWAEFTAL 150
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(TJ)

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2	615	44.0	233	2	S51761	BCL-X protein - rat	7.19e-98
3	615	44.0	233	2	L49056	bcl-x long - mouse	7.19e-98
4	587	42.0	233	2	A37332	transforming protein	4.11e-92
5	586	41.9	239	1	TVHUAI	transforming protein	6.59e-92
6	583	41.7	236	2	I67432	BCL-2 - rat (fragment	2.72e-91
7	579	41.4	236	2	I53744	gene bcl-2 protein -	1.80e-90
8	577	41.3	233	2	I67431	BCL-X-long - rat	4.62e-90
9	572	40.9	236	1	TVMSAI	transforming protein	4.89e-89
10	567	40.6	232	2	S24390	transforming protein	5.16e-88
11	543	38.9	214	2	I49057	bcl-x transmembrane d	4.13e-83
12	538	38.5	227	2	JE0203	apoptosis regulator b	4.32e-82
13	537	38.4	230	2	A47537	apoptosis regulator b	6.90e-82
14	511	36.6	206	1	D37332	transforming protein	1.33e-76
15	509	36.4	199	1	TVMSBI	transforming protein	3.39e-76
16	499	35.7	205	1	TVHUB1	transforming protein	3.59e-74
17	499	35.7	216	2	B37332	transforming protein	3.59e-74
18	402	28.8	154	2	I58194	gene bcl-2 protein -	9.58e-55
19	235	16.8	193	2	D47538	bcl-2-associated prot	7.46e-23
20	228	16.3	143	2	I38921	bcl-2-associated prot	1.37e-21
21	228	16.3	192	2	A47538	bcl-2-associated prot	1.37e-21
22	226	16.2	211	2	S58873	Bak protein - human	3.14e-21
23	225	16.1	133	2	I53295	bcl-2-associated prot	4.75e-21

CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/081,448
CC FILING DATE: 19930622
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5646008thrup, Thomas E.
CC REGISTRATION NUMBER: 33,268
CC REFERENCE/DOCKET NUMBER: ARCD090
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-744-0090
CC TELEFAX: 312-755-4489
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 233 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 233 AA; 26063 MW; 275311 CN;

Query Match 44.1%; Score 616; DB 1; Length 233;
Best Local Similarity 53.1%; Pred. No. 6.27e-44;
Matches 77; Conservative 30; Mismatches 36; Indels 2; Gaps 2;
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Db 145 SFGGALCVESVDKEMQVLVSRIAAMATYLNHLEPWIQENGWDTFVELYGNNAAESR 204
QY 101 LFGAALCAESVKNKEMPELVGQVQEWVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160
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QY 161 RLREG-N-WASVRTVLTGAVAGAL 183

RESULT 15
ID US-08-661-479-59 STANDARD; PRM; 233 AA.
XX xxxxxx
AC
XX
XX
XX
XX
DE Sequence 59, Application US/08661479
CC Sequence 59, Application US/08661479
CC Patent No. 5834209
CC GENERAL INFORMATION:
CC APPLICANT: KORSMEYER, Stanley J.
CC TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
CC TITLE OF INVENTION: REGULATOR
CC NUMBER OF SEQUENCES: 59
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/661,479
CC FILING DATE: 11-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/333,565
CC FILING DATE: 31-OCT-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15726A-000700
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 59:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 233 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: peptide
CC SEQUENCE 233 AA; 26049 MW; 275801 CN;

Query Match 44.1%; Score 616; DB 2; Length 233;
Best Local Similarity 53.1%; Pred. No. 6.27e-44;
Matches 77; Conservative 30; Mismatches 36; Indels 2; Gaps 2;
Db 85 AVKQALREAGDEFEELRYRAFSDLTSQLHTPGTAYQSFQVNVNELFRDGVNNGRIVAFF 144
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Db 145 SFGGALCVESVDKEMQVLVSRIAAMATYLNHLEPWIQENGWDTFVELYGNNAAESR 204
QY 101 LFGAALCAESVKNKEMPELVGQVQEWVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160
Db 205 KGQERFNWFLTGMTVAGVLLGSL 229
QY 161 RLREG-N-WASVRTVLTGAVAGAL 183

Search completed: Fri Jun 23 14:16:17 2000
Job time : 12 secs.

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121	VOEWMVAYLETRLADWTHSSGGWAEFTALYDGALEEARLRREGNWAASVRTLVTGAVALG	180
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181	ALVTVGAFPAASK	192
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AC		
XX		
DF		
XX		
XX		
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XX	Sequence 6, Application US/08798897	
CC	Patent No. 5789201	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Guastella, John	
CC	TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2	
CC	TITLE OF INVENTION: Homologue	
CC	NUMBER OF SEQUENCES: 53	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.	
CC	STREET: 1100 New York Avenue, N.W., Suite 600	
CC	CITY: Washington	
CC	STATE: DC	
CC	COUNTRY: USA	
CC	ZIP: 20005	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: US/08/798,897	
CC	FILING DATE: February 11, 1997	
CC	CLASSIFICATION: 435	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Esmond, Robert W.	
CC	REGISTRATION NUMBER: 32,893	
CC	REFERENCE/DOCKET NUMBER: 1483.0140001	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: 202-371-2600	
CC	TELEFAX: 202-371-2540	
CC	INFORMATION FOR SEQ ID NO: 6:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 192 amino acids	
CC	TYPE: amino acid	
CC	STRANDEDNESS: not relevant	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: protein	
SO	SEQUENCE 192 AA; 20701 MW; 181510 CN;	

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Db      61  SDAIAQLHVTGCSAQQRFTQVSDLELFGGGPNNGRLVAFVFTGAALCAESVKNKEMEPLVGG 121
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QY      122  VQWVAVLETRLADWTHSSGGWAEFTALYGDGALFEARRLRREGNWASVRTVLTGVAALG 181
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QY      182  ALVTVGGAFFASK 193

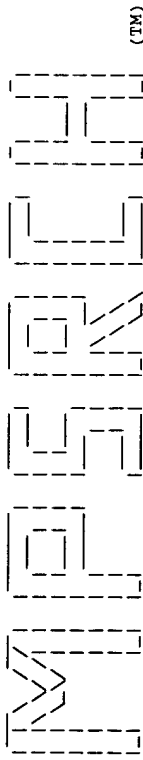
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DT      DT
XX      Sequence 5, Application US/08978523
DE      DE
XX      Sequence 5, Application US/08978523
CC      Patent No. 5883229
CC      GENERAL INFORMATION:
CC      APPLICANT: Guastella, John
CC      TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
CC      TITLE OF INVENTION: Homologue
CC      NUMBER OF SEQUENCES: 53
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC      STREET: 1100 New York Avenue, N.W., Suite 600
CC      CITY: Washington
CC      STATE: DC
CC      COUNTRY: USA
CC      ZIP: 20005
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/978,523
CC      FILING DATE: herewith
CC      CLASSIFICATION: 424
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/798,897
CC      FILING DATE: February 11, 1997
CC      CLASSIFICATION: 424
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Esmond, Robert W.
CC      REGISTRATION NUMBER: 32,893
CC      REFERENCE/DOCKET NUMBER: 1483.0140002
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 202-371-2600
CC      TELEFAX: 202-371-2540
CC      INFORMATION FOR SEQ ID NO: 5:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 192 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: not relevant
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 192 AA; 20689 MW; 183185 CN;

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Category	Count	Conservative	Mismatches	Indels	Gaps
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	Query Match	97.9%: score 1368:

Query Match 97.9%; Score 1368; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.58e-112;
Matches 189; Conservative 1; Mismatches 2; Indels 0



(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:16:05 2000; MasPar time 5.04 Seconds

Tabular output not generated. 552.912 Million cell updates/sec

>US-09-155-327B-7

Description: (1-193) from US09155327B.pep

Perfect Score: 1397

Sequence: 1 MATPASAPDTRALVADPVGY.....LTGVALGALVTVGAFASK 193

Scoring table: PAM 150

Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-issued

1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 30.708; Variance 142.172; scale 0.216

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
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3	1378	98.6	193	Sequence 3, Applicatio	1.90e-113
4	1378	98.6	193	Sequence 3, Applicatio	1.90e-113
5	1368	97.9	192	Sequence 6, Applicatio	1.58e-112
6	1368	97.9	192	Sequence 6, Applicatio	1.58e-112
7	1367	97.9	192	Sequence 5, Applicatio	1.95e-112
8	1367	97.9	192	Sequence 5, Applicatio	1.95e-112
9	616	44.1	233	PCT-US95-0 Sequence 24, Applicatio	6.27e-44
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15	616	44.1	233	Sequence 6, Applicatio	6.27e-44
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17	616	44.1	233	Sequence 14, Applicati	6.27e-44
18	587	42.0	233	Sequence 24, Applicati	6.27e-44
19	587	42.0	233	Sequence 23, Applicati	2.51e-41
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21	586	41.9	239	Sequence 10, Applicati	3.09e-41
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23	586	41.9	239	Sequence 10, Applicati	3.09e-41

24 586 41.9 239 1 US-08-112- Sequence 10, Applicati 3.09e-41
25 584 41.8 236 1 US-08-607- Sequence 22, Applicati 4.67e-41
26 584 41.8 236 4 PCT-US95-0 Sequence 20, Applicati 4.67e-41
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33 575 41.2 239 1 US-08-690- Sequence 4, Applicatio 2.99e-40
34 575 41.2 239 2 US-08-337- Sequence 12, Applicati 2.99e-40
35 575 41.2 239 1 US-08-661- Sequence 51, Applicati 2.99e-40
36 575 41.2 239 1 US-08-248- Sequence 12, Applicati 2.99e-40
37 575 41.2 239 3 US-09-113- Sequence 4, Applicatio 2.99e-40
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44 575 41.2 239 2 US-08-365- Sequence 15, Applicati 2.99e-40
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ALIGNMENTS

RESULT 1
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AC xxxxxx
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DT
DT
XX

Sequence 4, Application US/08798897

Sequence 4, Application US/08798897

Patent No. 5789201

GENERAL INFORMATION:

APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 193 AA; 20832 MW; 183365 CN;

Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
97044477

On Jul 7, 1999 this sequence version replaced gi:5866278.

Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: m5t@mail.nih.gov

Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA-No.

FEATURES
SOURCE

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/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pTT30-Pac (Pharmacia) with a modified
polylinker. Site.1: Not I; Site.2: Eco RI; The
NIH_BMAP_M_S3.1 library is a subcloned library of a
tagged normalized libraries from ten regions of individually
brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus) after a series of
subclonings to reduce the representation of cDNAs from
which ESTs had already been generated. The following
serially subcloned libraries were generated in this
process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1.
The subcloned library (NIH_BMAP_M_S3.1) was constructed
as follows: PCR-amplified cDNA inserts from NIH_BMAP_M_S2
clones from which 3' ESTs had been derived was used as a
driver in a hybridization with the NIH_BMAP_M_S2 library
in the form of single-stranded circles. The remaining
single-stranded circles (subcloned library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the
NIH_BMAP_M_S3.1 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)
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TAG_TISSUE=hippocampus
TAG_SEQ=TCAG."

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QY	221	cagcccgagcaacgcttccacocaggtttccgcagcaactttccaggggggcgcctaactggg	280		

Db	211	CGCGCTATCAGAGCTTTGAGCAGGTAGTGAATGAACCTCTTCGGGATGGAGTAAACTGGG	152
QY	281	gcgcctctggcattcttctcttgggctgcctctgtctgcagagtgtcaacaag	340
Db	151	GTCCGATCGTGGCCCTTTTCCTTTTGGCGGGGACATGTCGCTGGGAACGCTAGACAAG	92
QY	341	aaatggagccttctgtgggacaaactccagagatggatcgtggcctaccctggagacacgtc	400
Db	91	AGATCAGGATTATGTGTGAGTCGGATTGCAAGTTGGATGGCCACCTATCTGAATGACCACC	32
QY	401	tggctgactggtatccacagcagtgaggcggtcg	431
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LOCUS	AI401297/c		
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VERSION	AI401297.1	GI:4244384	30-MAR-1999
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SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 471)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	On Apr 7, 1998 this sequence version replaced gi:3035272.		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert_Strausberg@nih.gov		
	Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: M. Bento Soares, Ph.D.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	Clone Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbr/image/image.html		

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Seq primer: -40UP from Gibco
High quality sequence stop: 445.

FEATURES source

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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; single strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCGAATGGAGCGGCCGATTCGCTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized and was constructed by Bento Soares and M. Fátima Gonçalves.

BASE COUNT	91 a	173 c	130 g	77 t
ORIGIN	Soares and M. Fatima Ronaldo			

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Best Local Similarity
19.0%; Score 110.2; DB 46; Length 471;
59.5%; Pred. No. 5.6e-18;

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Db	284	GGGGAACATGGGCATCAGTGAGGACAGTGTCTACMGTCGCCGTGGCCTTGT	343
Qy	552	aactgtaggggcccttttttctagcaagt	581
Db	344	AACTGTANGGGCCCTTTTGTAGCAAGTG	373
RESULT	9		
LOCUS	W01420	437 bp	mRNA
DEFINITION	IMAGE:298187	5' similar to SW:BCUX_HUMAN Q07817	18-APR-1996
ACCESSION	W01420		
VERSION	W01420.1	GI:1273428	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.		
TITLE	The WashU-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	On Apr 14, 1993 this sequence version replaced gi:785898. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET High quality sequence stop: 383.		
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	/dev_stage="19 weeks"		
	/lab_host="DH10B (ampicillin resistant)"		
	/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TCCTACCAATCTGAAGTGGGAGCGCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHL19W."		
BASE COUNT	99 a	106 c	140 g
ORIGIN		89 t	3 others
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Qy	432	ggcgacttcacagctctatatacgggacggggccctggagcagcgcgtctgcgga	491
Db	261	GGCGAGTTCACAGCTCTATACGGTGTACAGCGCCCTGGAGGATCGCGGGCTCTGCGGGA	320
Qy	492	gggcaactgggcatgagtgacacagtggtgacggggccgtggcactggggccctggt	551
Db	321	GGGCACTGGGCATCAGTGAGGACAGTGTCTACMGTCGCCGTGGCCTTGT	380
Qy	552	aactgtaggggcccttttttctagcaagt	581
Db	381	AACTGTAGGGCCCTTGTGTAGCAAGTG	410
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DEFINITION	HS-5062_A2_G02.SP6E RPCI-11 Human Male BAC Library genomic clone Plate=638 Col=4 Row=M, genomic survey sequence.	GSS	13-MAR-1999
ACCESSION	A0401160		
VERSION	A0401160.1	GI:4412503	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)		
MEDLINE	99380589		
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 638 row: M column: 4 Seq primer: SP6 Class: BAC ends High quality sequence stop: 455.		
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	/sex="male"		
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Best Local Similarity	88.7%;	Pred. NO. 1.9e-21;	
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Qy 61 aggcctgagcagaagggttatgtctgtgagctggcctgggaaagccagccgagcgcac 120
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 Db 214 AAGCTGAGGAGAGAGGGGTATGTTGTGGAGCTGGCCCGGGGAGGGCCAGCAGCTGAC 273
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 Qy 121 ccgctgcaccagccatgcggctgctggagagagagtttgagaccctttccgcgcgcac 180
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 Db 274 CCGCTACACCAAGCATCGCGGCGAGCTGGAGATGAGTTCGAGACCCGCTTCCGCGCGCAC 333
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 Qy 181 ttctctgacctggcgcctcaactacagccagccagcagctcagccagcaacgcttcac 240
 |||||
 Db 334 TTCCTCGATCTGGAGCTCACTGCTGAGTGAACCCCGGCTCGGCCCAAGCAACGCTTCACC 393
 |||||
 Qy 241 cagggttccgcagcaactttccaaagggggcccttaactggg 280
 |||||
 Db 394 CAGGTCTCTGATGAACCTCTTCCAAAGGGGGCCCAACTGGG 433
 |||||

RESULT 4
 AW048567/c
 LOCUS
 DEFINITION UI-M-BH1-*alx-e-10-0-UI*.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone 18-SEP-1999
 UI-M-BH1-*alx-e-10-0-UI* 3', mRNA sequence.
 ACCESSION AW048567
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 431)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704477
 COMMENT On Feb 18, 1999 this sequence version replaced gi:4297581.
 Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mest@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES
 Source
 1. 431
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH1-*alx-e-10-0-UI*"
 /clone.lib="NIH_BMAP_M_S2"
 /dev_stage="27-32 days"
 /lab_host="DHI0B (Life Technologies)"
 /note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver

used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.

TAG_L1B=NIH_BMAP_M_S2
 TAG_TISSUE=corpus-striatum
 TAG_SEQ=ACGGC

BASE COUNT 105 a 131 c 85 g 110 t
 ORIGIN

Query Match 30.8%; Score 179.2; DB 64; Length 431;
 Best Local Similarity 98.4%; Pred. NO. 2.4e-35;
 Matches 181; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 250 gacgaactttccaagggggcccttaactgggcccgtcttctgtgacattcttctgttggg 309
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 Db 431 GACGAACCTTTCCAGGGGGCCCTAACTGGGCGCTCTGTGGCATCTTTGTCTTTGGG 372
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 QY 310 gctgcctctgtgtgagagtgctcaacaagaaatggagcctttggtgggacaagctccag 369
 |||||
 Db 371 GCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGTGGGACACAGTGCAG 312
 |||||
 QY 370 gattggatgctggcctacctgagagacacgtctggtgactggtatccacagcagtgccgc 429
 |||||
 Db 311 GATTGGATGTGGCCTTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGGGGC 252
 |||||
 QY 430 tggg 433
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 Db 251 TGGG 248

RESULT 5
 AW159063
 LOCUS
 DEFINITION za50h02.x1 Xenopus EST library Xenopus laevis cDNA clone za50h02
 5', mRNA sequence.
 ACCESSION AW159063
 VERSION
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 416)
 AUTHORS Schutz,K., de la Bastide,M., Huang,E.N., Nasciminto,L., Preston,R., Shah,R., Swaby,I., Shekher,M., Spiegel,L., Vil,M.D. and McCombie,W.R.

Expressed sequence tags from Xenopus
 Unpublished (1999)

On Jun 5, 1998 this sequence version replaced gi:3189433.
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org

Plate: za50 row: h column: 02
 Seq primer: M13 universal forward primer
 High quality sequence stop: 416.

FEATURES
 Location/Qualifiers
 1. 416

/organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="za50h02"
 /clone.lib="Xenopus EST library"
 /tissue_type="total brain tissue"
 /cell_line="W22-TGA"
 /dev_stage="tadpole"
 /note="Vector: Lambda Zap I; Site.1: XbaI; This library was supplied by Holly Cline (Cold Spring Harbor Labs)."

Db 531 ACTGGGGGCT 540

RESULT 2

AA596919

LOCUS

DEFINITION VO21f08.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1050567 5' similar to TR:E123735 R1 MRNA. ; , mRNA
sequence.

ACCESSION

AA596919

VERSION

AA596919.1

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 362)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

TITLE

The WashU-HHMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

On Dec 18, 1996 this sequence version replaced gi:1734345.

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:582143

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 334.

FEATURES

source

1..362

/organism="Mus musculus"

/strain="C3H"

/db_xref="taxon:10090"

/clone="IMAGE:1050567"

/clone_lib="Barstead mouse myotubes MPLRB5"

/cell_line="C2C12"

/lab_host="DH10B"

/note="Vector: p7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTACGAATCTGAAGTGGGAGCGCGCTTTTCTTTTCTTTTCTTTTCTTTT

3')]; double-stranded cDNA was ligated to Eco RI adaptors

[AATCGGATCTTG], digested with Not I and cloned into the

Not I and Eco RI sites of the modified p7T3 vector.

Library constructed by Bob Barstead. The C2C12 cell line

(available from ATCC, catalog # CRL-1772) differentiates

rapidly, forming contractile myotubes and producing

characteristic muscle proteins."

BASE COUNT

64 a 116 c 107 g 75 t

ORIGIN

QY 126 gacccaagccatcgggctgtgtgagacagctttgagacccgtttccgcgcacaccttc 185
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Db 149 GCACCAAGCCATGCTGCTGCTGGAGACAGAGTTTGAGACCCGTTTCGCCGCGACCTTCTC 208
|||||
QY 186 tgacctggcgcgtctagctacacgtgacccaggtcagccagcagcagcagcagcaggt 245
|||||
Db 209 TGAAGTGGCGCTCAGCTACAGCTAGCCAGGCTCAGCCAGGCTCAGCCAGGCTTACCAGGT 268
|||||
QY 246 ttccgacgaacttttccaagggggccctaactagggccgctctgtggcatttttctctt 305
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Db 269 TTCGAGCAACTTTTCCAGGGGGCCCTAACTGGGGCCGCTTTGTGGCATTTCTTTGCTT 328
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QY 306 tgggctgcccctgtgtgtgagagtgtaacaa 338
|||||
Db 329 TGGGGCTGCCCTGTGTGCTGAGAGTGTCACAAA 361
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RESULT 3

AW326901

LOCUS

DEFINITION

20104 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION

AW326901

VERSION

AW326901.1

KEYWORDS

EST.

SOURCE

Bos taurus.

ORGANISM

Bos taurus

REFERENCE

1 (bases 1 to 433)

Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,

Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and

Keele,J.W.

TITLE

Design and use of four pooled tissue normalized cDNA libraries for

EST discovery in cattle

JOURNAL

Unpublished (2000)

COMMENT

On Dec 20, 1995 this sequence version replaced gi:1133576.

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 20

and -mismatch 12 options.

PCR primers

Location/Qualifiers

1..433

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 2BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from testis, thymus,

semitendinosus muscle, longissimus muscle, pancreas,

adrenal, and endometrium."

BASE COUNT

80 a 142 c 143 g 68 t

ORIGIN

Query Match 39.4%; Score 228.8; DB 80; Length 433;

Best Local Similarity 88.6%; Pred. No. 8e-48;

Matches 248; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 atccgacccacccctcaacccagcacacacgcgctctagtgcactttagctat 60

|||||

Db 154 ATGGCGACCCCGCTCGGCCCGCCAGACACACGGGCTCTAGTGGCAGACTTTGTGGGTAT 213

|||||

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 4, 2000, 01:06:08 ; Search time 795.04 Seconds

(without alignments)

2962.018 Million cell updates/sec

Title: US-09-155-327B-8

Perfect score: 581

Sequence: 1 atgcgcacccagcctcaac.....gcctttttgctagcaagtg 581

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
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105: gb_gss12:*
106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	#	Query	Result
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;; COUNTRY: USA
;; ZIP: 94306
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/365,486A
;; FILING DATE: 23-DEC-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sholtz, Charles K.
;; REGISTRATION NUMBER: 38,615
;; REFERENCE/DOCKET NUMBER: 8255-0018
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 324-0880
;; TELEFAX: (415) 324-0960
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5086 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: human bcl-2 cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1459..2178
;; US-08-365-486A-14

Query Match 21.5%; Score 125; DB 3; Length 5086;
Best Local Similarity 58.9%; Pred. No. 3.7e-26;
Matches 215; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 91 gctgggctggggaagccagccagccgagccgctgacccaagccatgcgggctgctgga 150
DB 1702 GCGGGGCTGCTCAGCCCGGTCACCTGTGCTCCACCTGGCCCTCCGCGCAAGCCGGC 1761

QY 151 gacgagttgagaccgtttccgcgcaccttctgtacctggcgcctcagctacacgtg 210
DB 1762 GACGACTTCTCCGCGGCTACCGCGGCGACTTCGCCGAGATGCCAGCAGTGCACCTG 1821

QY 211 accccaggtcagccagcaagcgtttccaccaggtttccagcaagcgtttccagcaggttcc 270
DB 1822 ACGCCCTTACCGCGCGGGACGCTTTTGCACGGTGGTGGGAGAGTCTTTCAGGACGGG 1881

QY 331 gtcacaaagaatgagcctttgtgggacagtgattggatcgtggcctacacgtg 390
DB 1942 GTCAACCGGGAGATGTCGCCCTGGTGACACATCGCCCTGTGGATGACTGAGTACCTG 2001

QY 391 gagacacgtcgtgactggtatccacagcagtgccgagtgccgagtgccgagtgccgagtgcc 450
DB 2002 AACCGGACCTGCACACCTGGATCCAGGATTAACGGAGGCTGGGATGCTTTGTGGAAGC 2061

QY 451 tacgg 455
DB 2062 TACGG 2066

RESULT 13

US-09-080-285-19
; Sequence 19, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:

;; APPLICANT: Reed, John
;; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
;; NUMBER OF SEQUENCES: 29
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/080,285
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/465,485
;; FILING DATE: 05-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/124,256
;; FILING DATE: 20-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/840,716
;; FILING DATE: 21-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/288,692
;; FILING DATE: 22-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fortney, Andrew D.
;; REGISTRATION NUMBER: 34,600
;; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (408) 436-2070
;; TELEFAX: (408) 436-2075
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5086 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-09-080-285-19

Query Match 21.5%; Score 125; DB 5; Length 5086;
Best Local Similarity 58.9%; Pred. No. 3.7e-26;
Matches 215; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 91 gctgggctggggaagccagccagccgagccgctgacccaagccatgcgggctgctgga 150
DB 1702 GCGGGGCTGCTCAGCCCGGTCACCTGTGCTCCACCTGGCCCTCCGCGCAAGCCGGC 1761

QY 151 gacgagttgagaccgtttccgcgcaccttctgtacctggcgcctcagctacacgtg 210
DB 1762 GACGACTTCTCCGCGGCTACCGCGGCGACTTCGCCGAGATGCCAGCAGTGCACCTG 1821

QY 211 accccaggtcagccagcaagcgtttccaccaggtttccagcaagcgtttccagcaggttcc 270
DB 1822 ACGCCCTTACCGCGCGGGACGCTTTTGCACGGTGGTGGGAGAGTCTTTCAGGACGGG 1881

QY 331 gtcacaaagaatgagcctttgtgggacagtgattggatcgtggcctacacgtg 390
DB 1942 GTCAACCGGGAGATGTCGCCCTGGTGACACATCGCCCTGTGGATGACTGAGTACCTG 2001

QY 391 gagacacgtcgtgactggtatccacagcagtgccgagtgccgagtgccgagtgccgagtgcc 450

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,704
; FILING DATE: 18-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO:1:
; LENGTH: 4825
5459251-1

Query Match      21.5%; Score 125; DB 7; Length 4825;
Best Local Similarity 58.9%; Pred. No. 3.7e-26;
Matches 215; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 91 gctgggcttggagagccgcttccgcgcgaccccttctctgacccgtgacccgtcagctacacgtg 210
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Db 1702 gcgagcttctccgcgcgtaccgcgcgacttcgcgcgagatgtccagccagctgcacctg 1821
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 211 acccaggtcagccagcaagcctcaccaggttccagcaaacatttccaaaggggc 270
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Db 1822 agccctccaccgcgcgggagccttgcacggtggtggagagctcttcaggacggg 1881
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 271 cctaaactggggcgtcttggcattcttcttggggcgtgcctgtgtgctgagagt 330
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1882 gtgaactggggagagattggcctcttcttggatcggtgggtcatgtgtgtggagagc 1941
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 331 gtcaacaaagaatggagccttgggtgggacaaagtccaggatttgatcgtggcctacctg 390
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 391 gagacagctcgtgactggatccacagcagtcagtcggcgtggcggaattccacagctcta 450
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Db 2002 aaccggcactgcacacctggatccaggataacaggagctggatggctttgtggaactg 2061
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QY 451 tacgg 455
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Db 2062 tacgg 2066

RESULT 11
US-08-465-485A-19
; Sequence 19, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; CITY: 1755 S. Jefferson Davis Hwy., Suite 400
; STATE: Arlington
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-465-485A-19

Query Match      21.5%; Score 125; DB 3; Length 5086;
Best Local Similarity 58.9%; Pred. No. 3.7e-26;
Matches 215; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 91 gctgggcttgggagggccagccgcgcgacccgctgcaccaagccatcgcggtgctgga 150
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Db 1702 GCGGGGCTGGGCTCAGCCGGTGCACCTGTGTGTCCACCTGGCCCTCCGCAAGCGGC 1761
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QY 151 gacgagtttggagacccttccgcgcgcaacttctgaactggtgcgcgtcagctacacgtg 210
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1762 GACGACTTCTCCCGCCCTACCGCGCGACTTCGCCGAGATGTCCACCGAGCTGCACCTG 1821
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 211 acccaggtcagccagcaacgcttccaccaggttccgacaaactttccaaaggggc 270
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1822 ACGCCCTTACCAGCGCGGACGCTTTGCCACGGTGTGGAGGAGCTCTTCAGGGACGGG 1881
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 271 cctaactggggcgtcttggcattcttcttgggtggcgtccctgtgtgtgagagt 330
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1882 GTGAACCTGGGGAGAGATTGTGGCCTCTTTGAGTTCGGTGGGTTCATGTGTGTGGAGAGC 1941
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 331 gtcaacaaagaatggagccttgggtgggacaaagtccaggattggatcgtggcctacctg 390
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1942 GTCAACCGGGAGATGTGCCCCCTGGTGGGACAAACATCCGCTGTGGATGACTGAGTACCTG 2001
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 391 gagacagctcgtgctgactggatccacagcagtcagtcggcgtggcggaattccacagctcta 450
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2002 AACCGGACCTGCACACCTGTGATCCAGGATACGGAGGCTGGGATGCCCTTTGTGGAACCTG 2061
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QY 451 tacgg 455
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Db 2062 TACGG 2066

RESULT 12
US-08-365-486A-14
; Sequence 14, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
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TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..717
; US-08-465-485A-20

Query Match 21.5%; Score 125; DB 3; Length 717;
Best Local Similarity 58.9%; Pred. No. 1.8e-26;
Matches 215; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 91 gctggcctgggaagccagccgagccgctgcacacgagccgctgctgga 150
Db 244 GCGGGCCCTGCGCTCAGCCCGGTGCCACCTGTGTCCACCTGGCCCTCCGCCAAGCCGCG 303
QY 151 gacgagttgagaccgtttccgcgcgacccctctctgacccgtgcgctcagctacacgtg 210
Db 304 GACGACTTCTCCCGCGCTACCGCGGCGACTTCCGCGGAGATGTCCAGCCAGCTGCACCTG 363
QY 211 acccaggtcagccagcaacgcttcacccaggtttccgacgaaacttttccaagggg 270
Db 364 ACGCCCTTACCGCGGGGAGCGCTTCCACGCTGTGGAGGAGCTCTTCAGGAGCGGG 423
QY 271 cctaactgggcccgtctgtgacattcttctgtgggctgcccctgtgtgctgagagt 330
Db 424 GTGAACCTGGGAGAGATGTGCGCCCTCTTGTGCTGGGTGGGTCATGTGTGTGGAGAGC 483
QY 331 gtcaacaagaatggagccctgtgtgggacaaagtcagagattggatggcctacctg 390
Db 484 GTCAACCGGAGATGTGCGCCCTGTGGACAAATCAGCCCTGTGGATGACTGAGTACCTG 543
QY 391 gagacagctgtgactgagatcacagcagtgagcgtggcgtggcggaacttcacagctcta 450
Db 544 ACCGGCACTGCACACCTGGATCCAGGATACACGAGGCTGGGATGCTTTGTGGAACTG 603
QY 451 tacgg 455
Db 604 TACGG 608

RESULT 9
US-09-080-285-20
; Sequence 20, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..717
; US-09-080-285-20

Query Match 21.5%; Score 125; DB 5; Length 717;
Best Local Similarity 58.9%; Pred. No. 1.8e-26;
Matches 215; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 91 gctggcctgggaagccagccgagccgctgcacacgagccgctgctgga 150
Db 244 GCGGGCCCTGCGCTCAGCCCGGTGCCACCTGTGTCCACCTGGCCCTCCGCCAAGCCGCG 303
QY 151 gacgagttgagaccgtttccgcgcgacccctctctgacccgtgcgctcagctacacgtg 210
Db 304 GACGACTTCTCCCGCGCTACCGCGGCGACTTCCGCGGAGATGTCCAGCCAGCTGCACCTG 363
QY 211 acccaggtcagccagcaacgcttcacccaggtttccgacgaaacttttccaagggg 270
Db 364 ACGCCCTTACCGCGGGGAGCGCTTCCACGCTGTGGAGGAGCTCTTCAGGAGCGGG 423
QY 271 cctaactgggcccgtctgtgacattcttctgtgggctgcccctgtgtgctgagagt 330
Db 424 GTGAACCTGGGAGAGATGTGCGCCCTCTTGTGCTGGGTGGGTCATGTGTGTGGAGAGC 483
QY 331 gtcaacaagaatggagccctgtgtgggacaaagtcagagattggatggcctacctg 390
Db 484 GTCAACCGGAGATGTGCGCCCTGTGGACAAATCAGCCCTGTGGATGACTGAGTACCTG 543
QY 391 gagacagctgtgactgagatcacagcagtgagcgtggcgtggcggaacttcacagctcta 450
Db 544 ACCGGCACTGCACACCTGGATCCAGGATACACGAGGCTGGGATGCTTTGTGGAACTG 603
QY 451 tacgg 455
Db 604 TACGG 608
RESULT 10
5459251-1
; Patent No. 5459251
; APPLICANT: Tsujimoto, Yoshida; Croce, Carlo A.
; TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
; SEQUENCES
; NUMBER OF SEQUENCES: 4

QY 128 accaagccatcgccggctgctggagacagagtttgagaccccgctttccgcccgaaccttctctg 187
Db 394 AGCAAGCGCTGAGGGAGCGGACGAGTTTGAACCTGCGGTACCGCGGGCATTTCAGTG 453
QY 188 acctggccgtcagctacagtcagccagcagctcagccagcaacccagcttt 247
Db 454 ACCTGACATCCAGCTCCACATCACCCAGGAGCAGCATATCAGAGCTTTGAACAGGTAG 513
QY 248 ccgacgaacttttccaaagggccctaaactggggccgcttttggccattcttctgtt 307
Db 514 TGAATGAACCTCTCCGGGATGGGTAACCTGCGATGCGCTTTTCCTCTCG 573
QY 308 gggctgcccctgtgctgagagtgctcaacaagaataaggagcccttggggacaagtcc 367
Db 634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGACGGCG 693
QY 428 gctggcgagctcacagctctatagggagcgggccctggagcagcagcgctctgc 487
Db 594 GCTGGGATACTTTGTGGAACTCTATGGGAACAATGACGAGCCGCGAGAGCCGAAAGGCC 753
QY 488 gggagggcaactggcgatgagtcacagctggtgacggggggcg 532
Db 754 AGGAACGCTTCAACCGCTGCTCTGACGGGCATGACTGTGGCG 798

RESULT 7

PCT-US94-07089-6
; Sequence 6, Application PC/TUS9407089
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07089
; FILING DATE: CONCURRENTLY FILED
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/081,448
; FILING DATE: 22 JUNE 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; PCT-US94-07089-6

Query Match 23.2%; Score 134.6; DB 6; Length 926;
Best Local Similarity 58.3%; Pred. No. 4e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
QY 128 accaagccatcgccggctgctggagacagagtttgagaccccgctttccgcccgaaccttctctg 187
Db 394 AGCAAGCGCTGAGGGAGCGGACGAGTTTGAACCTGCGGTACCGCGGGCATTTCAGTG 453
QY 188 acctggccgtcagctacagtcagccagcagctcagccagcaacccagcttt 247
Db 454 ACCTGACATCCAGCTCCACATCACCCAGGAGCAGCATATCAGAGCTTTGAACAGGTAG 513
QY 248 ccgacgaacttttccaaagggggccctaaactggggccgcttttggccattcttctgtt 307
Db 514 TGAATGAACCTCTCCGGGATGGGTAACCTGCGATGCGCTTTTCCTCTCG 573
QY 308 gggctgcccctgtgctgagagtgctcaacaagaataaggagcccttggggacaagtcc 367
Db 574 GCGGGGCATGTCGCTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGTGATCGGATCG 633
QY 368 agattgagctggccctacactggagacagctctgctgactgagtcacacagcagtg 427
Db 634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGACGGCG 693
QY 428 gctggcgagctcacagctctatagggagcgggccctggagcagcagcgctctgc 487
Db 694 GCTGGGATACTTTGTGGAACTCTATGGGAACAATGACGAGCCGCGAGAGCCGAAAGGCC 753
QY 488 gggagggcaactggcgatgagtcacagctggtgacggggggcg 532
Db 754 AGGAACGCTTCAACCGCTGCTCTGACGGGCATGACTGTGGCG 798

RESULT 8

US-08-465-485A-20
; Sequence 20, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

Qy	421	agtgcgcgctggcggaacttcaacagctctatacgggacgaggccctggagagacacagc	480
Db	421	AGTGGGGCTGGCGGAGATTCACAGCTCTATACGGGACGGGGCCCTGTGAGGAGCGCGG	480
Qy	481	cgctcgggaggggaactgggcatgagtggacacagtggtgacggggccctggcaactg	540
Db	481	CGTCTCGGGAGGGGAACCTGGGCATCATGTGAGACAGTCTGACGGGGCCCTGGCACTG	540
Qy	541	ggggccctggtaaactgtaggggccttttttgcctagcaag	579
Db	541	GGGGCCCTGTTAACTGTAGGGGCGCTTTTGTGTAGCAAG	579

RESULTS

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US-08-081-448-5
; Sequence 5, Application US/08081448
; Patent No. 5646008
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5646008th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: 19930622
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646008thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; PS-08-081-448-5

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	Query Match	23.2%	Score 134.6	DB 1	Length 926	
	Best Local Similarity	58.3%	Pred. No. 4e-29			
	Matches 236	Conservative 0	Mismatches 169	Indels 0	Gaps	
Qy	128	accaagccatgcgggctgctggagacgaggtttgagaccggtttccgcgcacaccttctctg	187			
Db	394	AGCAAGCGCTGAGGGAGCGAGCGAGGTTTGAATGCGGTCACCGCGGGCATTCAGTG	453			
Qy	188	acctggcgctcgactacagtgacccccaggctcagccagcaacgcttccaccaggttt	247			
Db	454	ACCTGACATCCGACTCCACATCACCCCGAGGACAGCATATCAGAGCTTTGAACAGGTAG	513			
Qy	248	ccgacgaacttttccaaagggggccctaactcggggcgctcttggtggcatctctttgtctcttg	307			

514	Db	TGAATGAACCTCTTCCGGGATGGGGTAAACATGGGGTGCATTTGGCGCTTTTCTCCTCG	573
308	Qy	gggctgcccctgtgtctgagagatgtcaacaagaataatgagcctttgggtggacaagtcc	367
574	Db	CGSGGGCACTGTGCGTGGAAAGCGTAGACAAGCAGATGCAGGTATTGGTTCAGTCGATCG	633
368	Qy	aggattggatctgtggccatacctggagacaagctctggctgactggatccacagcagtgggcg	427
634	Db	CAGCTTGGATGGCCACTTACTCAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG	693
428	Qy	gctggggcggaacttcacagctctctatcagggagcggggccctggaggagcgcacggcgctctgc	487
694	Db	GCTGGGATACTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGACCCGAAGGGCC	753
488	Qy	ggaggggcaactgggcatgagtgagcacagtgtgtacggggggcg	532
754	Db	AGGAACGCTTCAACCGCTGGTCTCTACGGGCATGACTTGGCGG	798

RESULT 6

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US-08-470-670A-6
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B. B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
US-08-470-670A-6

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Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 4e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-08-798-897-2

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Query Match      85.6%; Score 497.4; DB 2; Length 579;
Best Local Similarity 91.2%; Pred. No. 3e-131;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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QY 1 atgcacacccagcctcaacccagacacacgcgctctagtggtgacttttaggtat 60
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DB 1 ATGCGACCCAGCCTCGGCCCCAGACACACGCGCTCTGTGGAAGACTTTGTAGTTAT 60

QY 61 agcttagcagaaggttatctctgagctggcctggggaagccagcccgac 120
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DB 61 AAGCTGAGGAGAAGGTTATGCTGTGAGCTGGCCCGGAGGCGCCAGCAGCTGAC 120

QY 121 ccgctgcacacacgcatcggtgctgagacgagttgagaccgtttccgcgcac 180
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DB 121 CCATGCACCAAGCCATCGGCGAGCTGCATGTGACCCAGGCTCAGCCCAACAGCTCACC 180

QY 181 ttcttgacctggcctacgctacacgctgacccagctcagccagcaacgctcacc 240
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DB 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACAGCTCACC 240

QY 241 caggtttccagcaacttttccaaaggggcccctaaactgagcgccttctgtggtat 300
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DB 241 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCGCCCTTGTAGCCCTCTTT 300

QY 301 gtctttgggctgcctgtgtgctgagagtgatcaacaaagaaatggagccttgggtgga 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 GTCTTTGGGGCTGCATGTGCTGAGAGTGTCAACAAGAGATGGAACCATGTTGGGA 360

QY 361 caagtcaggattggatcgctgacctggagacacgctctggtgactggatccacagc 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 CAAATGCAGGAGTGGATGGTGGCTACCTTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

QY 421 agtggcggtggcggaacttcacagctctatcaggggaagggcccctggagacacag 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 421 AGRGGGGGCTGGCGAGTGTACAGCTCTATACGGGGAGCGGGCCCTGGAGAGCGGG 480

QY 481 cgtctcggggagggcaactggcgatgagcagtggtgacggtgaggggcccgtggcactg 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 CGTCTCGGGGAGGGGAACCTGGGCATCAGTGTGAGGACAGTGTCTACGGGGCCCTGGGCATG 540

QY 541 ggggcccctgtaactgtaggggcccttttttctgtaagaag 579
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DB 541 GGGGCCCTGTGAACCTGTAGGGCCCTTTTGTGTAGCAAG 579

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RESULT 4
US-08-978-523-2
; Sequence 2, Application US/08978523
; Patent No. 5883229

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; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-08-978-523-2

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Query Match      85.6%; Score 497.4; DB 3; Length 579;
Best Local Similarity 91.2%; Pred. No. 3e-131;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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QY 121 ccgctgcacacacgcatcggtgctgagacgagttgagaccgttttccgcgcac 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CCATGCACCAAGCCATCGGCGAGCTGCATGTGAGTGTGAGACCCCGCTCCGCGGACC 180

QY 181 ttcttgacctggcctacgctacacgctgacccagctcagccagcaacgctcacc 240
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DB 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACAGCTTACC 240

QY 241 caggtttccagcaacttttccaaaggggcccctaaactgagcgccttctgtggtat 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCGCCCTTGTAGCCCTCTTT 300

QY 301 gtctttgggctgcctgtgtgctgagagtgatcaacaaagaaatggagccttgggtgga 360
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DB 301 GTCTTTGGGGCTGCATGTGCTGAGAGTGTCAACAAGAGATGGAACCATGTTGGGA 360

QY 361 caagtcaggattggatcgctgacctggagacacgctctggtgactggatccacagc 420
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DB 361 CAAATGCAGGAGTGGATGGTGGCTACCTTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

QY 421 agtggcggtggcggaacttcacagctctatcaggggaagggcccctggagacacag 480
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DB 421 AGRGGGGGCTGGCGAGTGTACAGCTCTATACGGGGAGCGGGCCCTGGAGAGCGGG 480

QY 481 cgtctcggggagggcaactggcgatgagcagtggtgacggtgaggggcccgtggcactg 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 CGTCTCGGGGAGGGGAACCTGGGCATCAGTGTGAGGACAGTGTCTACGGGGCCCTGGGCATG 540

QY 541 ggggcccctgtaactgtaggggcccttttttctgtaagaag 579
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 541 GGGGCCCTGTGAACCTGTAGGGCCCTTTTGTGTAGCAAG 579

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Qy	61	agcgtcagggcagaaggggttatctctcgaagctcgtggcctgggaaagggccagccgccac	120
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Qy	121	ccgctgcaccaaagccatcggggctcgtcgagacagattcgagaccggtttccgcgcgcacc	180
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Qy	181	ttctctgacctggccgctcagctctacagtcgaccccaagctcgacccagcaacgcttcacc	240
Db	181	TTCTCTGACCTGGCCGCTCAGCTTACAGTGACCCAGGCTCAGCCGACGCAACGCTTCACC	240
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Qy	361	caagtcacagatggatcgtggcctaccctggagacacgctcgtcgtcagctggatccacagc	420
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RESULT 2

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US-08-978-523-1
: Sequence 1, Application US/08978523
: Patent No. 5883229
: GENERAL INFORMATION:
: APPLICANT: Guastella, John
: TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
: TITLE OF INVENTION: Homologue
: NUMBER OF SEQUENCES: 53
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 New York Avenue, N.W., Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/978,523
: FILING DATE: herewith
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/798,897
: FILING DATE: February 11, 1997
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Esmond, Robert W.
: REGISTRATION NUMBER: 32,893
: REFERENCE/DOCKET NUMBER: 1483.0140002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-978-523-1

Query Match          93.0%; Score 540.6; DB 3; Length 579;
Best Local Similarity 95.9%; Pred. No. 2.1e-143;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps

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   |||
Db 121 CCGCTGCACCAACCCATGCGGGCAGCTGGAGACAGAGTTTGAGACCCCGCTTCCGGCGCACC 180

Qy 181 ttctctgacctggcgctcagctacacgtgacccagcgtcagcccgagcaacgcttcacc 240
   |||
Db 181 TTCTCTGACCTGGCCGCTCAGCTACAGCTGACCCAGGCTCAGCCAGCAACGGTTCCACC 240

Qy 241 caggcttcgcagcaaatctttccaaagggggccctaaactagggccgctctgttggaattcttt 300
   |||
Db 241 CAGGTTTCCGACGAACCTTTTCCAAGGGGGCCCAACTGGGGCCGCTCTGTGGCAATCTTT 300

Qy 301 gtctttggggctccctgtgtgctgagagtgctcaacaagaaatggagcctttgtgtggga 360
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РЕСПУБЛИКА

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RESOL: 3
US-08-798-897-2
; Sequence 2, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; NUMBER OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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2	540.6	93.0	579	3	US-08-978-523-1	Sequence 1, Appli
3	497.4	85.6	579	2	US-08-798-897-2	Sequence 2, Appli
4	497.4	85.6	579	3	US-08-978-523-2	Sequence 2, Appli
5	134.6	23.2	926	1	US-08-081-448-5	Sequence 5, Appli
6	134.6	23.2	926	3	US-08-470-670A-6	Sequence 6, Appli
7	134.6	23.2	926	6	PCR-US94-07089-6	Sequence 6, Appli
8	125	21.5	717	3	US-08-465-485A-20	Sequence 20, Appli
9	125	21.5	717	5	US-09-080-285-20	Sequence 20, Appli
10	125	21.5	4825	7	5459251-1	Patent No. 5459251
11	125	21.5	5086	3	US-08-465-485A-19	Sequence 19, Appli
12	125	21.5	5086	3	US-08-365-486A-14	Sequence 14, Appli
13	125	21.5	5086	5	US-09-080-285-19	Sequence 19, Appli
14	125	21.5	5086	6	PCR-US93-05651-4	Sequence 4, Appli
15	125	21.5	5086	6	PCR-US93-06251-2	Sequence 2, Appli
16	125	21.5	5104	7	5506344-1	Patent No. 5506344
17	123.4	21.2	760	2	US-08-405-702A-11	Sequence 11, Appli
18	123.4	21.2	1846	3	US-08-365-486A-16	Sequence 16, Appli
19	120.2	20.7	1274	3	US-08-470-670A-1	Sequence 1, Appli
20	120.2	20.7	1274	6	PCR-US94-07089-1	Sequence 1, Appli
21	120.2	20.7	1303	1	US-08-081-448-1	Sequence 1, Appli
22	119	20.5	615	3	US-08-465-485A-22	Sequence 22, Appli
23	119	20.5	615	5	US-09-080-285-22	Sequence 22, Appli
24	119	20.5	911	6	PCR-US93-06251-3	Sequence 3, Appli
25	115.8	19.9	831	7	5459251-3	Patent No. 5459251
26	115.8	19.9	831	7	5506344-4	Patent No. 5506344
27	74.8	12.9	623	7	5506344-3	Patent No. 5506344

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Qy 401 tgcgtgactgataccacagcagtgccgctggcgagactcacagctctatacagggagc 460
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Qy 521 tgacgggggcccgtgg 535
Db 665 TGACTCTAGCTGGGG 679

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LOCUS Sus scrofa mRNA for anti-apoptotic Bcl-xL.
DEFINITION Sus scrofa mRNA for anti-apoptotic Bcl-xL.
ACCESSION AJ001203
VERSION AJ001203.1 GI:3288631
KEYWORDS apoptosis.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Suiformes; Suina; Suidae; Sus.
1 (bases 1 to 752)
Direct Submission
Bartling,B.
Submitted (13-JAN-1998) Bartling B., Institute of Pathophysiology,
Martin Luther University, Magdeburger Strasse 18, 06097 Halle,
GERMANY
2 (bases 1 to 752)
Bartling,B., Hoffmann,J., Holtz,J., Schulz,R., Heusch,G. and
Darmer,D.
Expression of apoptosis-associated genes in hibernating and stunned
myocardium of pig
Unpublished
Location/Qualifiers
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44..745
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Best Local Similarity 56.8%; Pred. No. 1.6e-21;
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Job time: 16645 sec

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QY 185 ctgacctggcgcctgactacacgtgacccaggtcagccagcaacgcttcaccagg 244

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QY 425 cgcgctggcgacttcacagctctatcgaggagcggggccctgagacgcagcgtc 484

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RESULT 11
AR054021

LOCUS AR054021 926 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 6 from patent US 5834309.

ACCESSION AR054021

VERSION AR054021.1 GI:5978883

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT 220 a 249 c 264 g 193 t

ORIGIN

Query Match 23.2%; Score 134.6; DB 5; Length 926;

Best Local Similarity 58.3%; Pred. No. 1.2e-21;

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QY 188 acctggcgcctgactacacgtgacccaggtcagccagcaacgcttcaccagttt 247

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DB 574 GCGGGCACTGTGCGTGAAGAGCGTAGACAAGGAGATGTCAGGTATTGGTGTAGTCGATCG 633

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DB 694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAANTGCACAGCCGAGAGCCGAAAGGGCC 753

QY 488 gggagggcaactgggcatgagtgagcacagtggtgacggggccg 532

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RESULT 12

IS2011

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY 128

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QY 188

DB 454

QY 248

DB 514

QY 308

DB 574

QY 368

DB 634

QY 428

DB 694

QY 488

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RESULT 9
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ACCESSION X82462
VERSION X82462.1 GI:575421
KEYWORDS xrl gene.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
REFERENCE 1 (bases 1 to 749)
AUTHORS Cruz-Reyes, J. and Rata, J.R.
TITLE Cloning, characterization and expression of two Xenopus bcl-2-like
cell-survival genes
JOURNAL Gene 158 (2), 171-179 (1995)
MEDLINE 95331613
REFERENCE 2 (bases 1 to 749)
AUTHORS Cruz-Reyes, J.A.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1994) J.A. Cruz-Reyes, National Institute of
Medical Research, NIMR/MRC Mill Hill, The Ridgeway Road, London NW7
1AA, UK
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source Location/Qualifiers
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3..689
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/protein_id="CAA57845.1"
/db_xref="GI:1334682"
/db_xref="SWISS-PROT:Q91827"
/translation="LNPKKKNGKNGKREKOHETGNTIFRSPDKYLTEOGWMAQS
DLGSRLVEDLVKLCORSIVPEPSCAASALHSAMRAAGDDEFEFRQAFSEISTQ
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MVTYLEDNRDWFQSGNGWNGFLTYGDGAIEBARQREGNWASLTKVLTGVALGAL
MTVGALFASK"
BASE COUNT 203 a 146 c 224 g 176 t
ORIGIN

Query Match 40.2%; Score 233.8; DB 4; Length 749;
Best Local Similarity 68.1%; Pred. No. 1.2e-44;
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QY 121 ccgctgcaacgaacgctgagctgagagagagttttagaccctttccgcgcacc 180
Db 121 CCACTGCACCAAGCCATGCGGGAGCTGGAGATGAGTTCAGACCCCTTCCGGCGCACC 180
QY 181 ttctctgacctggcgcctcagctacacgtgacccagcgtcagcccgcaacgcttccacc 240
Db 181 TTCCTGATCTGGCGCTCAGCTCATGTGACCCAGCTCAGGCCAACCAACGCTTCAACC 240
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QY 301 gctcttgggctccctgtgtgctgagtggtcaacaaagaaatggagccttggtagga 360
Db 301 GTCCTTTGGGGCTGACATGTGTGCTGAGAGTGTCAACAGGAGATGAACCACTGGTGGGA 360
QY 361 caagtcaggagattgattgctgctacactgagacacagcttggctgactgattccacagc 420
Db 361 CAAGTGCAGGAGTGGATGGTGGCTTACTGTGAGACGCGGCTGGCTGACTGCATCCACAGC 420
QY 421 agtggcggctggcggacttcaacgctctatacgggacggggccctggaggagcagcg 480
Db 421 AGTGGGGCTGGGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGAGCGCGG 480
QY 481 cgtctcgggagggcaactggcgtgagtgagtgagcagctgtgacggggccgtggcactg 540
Db 481 CGTTCGGGGAGGGAACTGGGCTATGAGTGTGAGGACATGTGACGGGGCGGCTGGCACTG 540
QY 541 ggggcccgttaactgtaggggccccttttctagcagaag 579
Db 541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTCTGTAGCAAG 579

RESULT 8
CNS0000B 196287 bp DNA PRI 27-OCT-1999
LOCUS Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-124D2 of
DEFINITION RPI-11 library from chromosome 14 of Homo sapiens (Human),
complete sequence.
ACCESSION AL049829 GI:6138746
VERSION AL049829.3 GI:6138746
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 196287)
Genoscope.
Direct Submission
Submitted (26-OCT-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT On Oct 28, 1999 this sequence version replaced gi:4972127.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continue. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage, etc.XX.
FEATURES
source /
Location/Qualifiers
1..196287
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/clone_lib="RPI-11"
/clone="R-124D2"
78257..78396
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/note="matching EMBL:AA908790; Identified using the e-PCR
software (G. Schuler)"
80431..80564
/standard_name="AA167748"

QY 121 ccgctgcaacgaacgctgagctgagagagagttttagaccctttccgcgcacc 180
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QY 181 ttctctgacctggcgcctcagctacacgtgacccagcgtcagcccgcaacgcttccacc 240
Db 181 TTCCTGATCTGGCGCTCAGCTCATGTGACCCAGCTCAGGCCAACCAACGCTTCAACC 240
QY 241 caggtttccgcagcaattttccaaagggggccctaaactggggccgtctgtggattttt 300
Db 241 CAGGTCTCCGATGAACATTTTCAAGGGGGGCCCAACTGGGGCCGCTGTAGCTTCTTT 300
QY 301 gctcttgggctccctgtgtgctgagtggtcaacaaagaaatggagccttggtagga 360
Db 301 GTCCTTTGGGGCTGACATGTGTGCTGAGAGTGTCAACAGGAGATGAACCACTGGTGGGA 360
QY 361 caagtcaggagattgattgctgctacactgagacacagcttggctgactgattccacagc 420
Db 361 CAAGTGCAGGAGTGGATGGTGGCTTACTGTGAGACGCGGCTGGCTGACTGCATCCACAGC 420
QY 421 agtggcggctggcggacttcaacgctctatacgggacggggccctggaggagcagcg 480
Db 421 AGTGGGGCTGGGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGAGCGCGG 480
QY 481 cgtctcgggagggcaactggcgtgagtgagtgagcagctgtgacggggccgtggcactg 540
Db 481 CGTTCGGGGAGGGAACTGGGCTATGAGTGTGAGGACATGTGACGGGGCGGCTGGCACTG 540
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Db 541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTCTGTAGCAAG 579

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/standard_name="AA007328"
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software (G. Schuler)"
107753..107946
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software (G. Schuler)"
107991..108176
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software (G. Schuler)"
128383..128521
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software (G. Schuler)"
128415..128539
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138457..138733
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software (G. Schuler)"
138504..138653
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software (G. Schuler)"
138563..138642
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/note="matching EMBL:M78986; Identified using the e-PCR
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138563..138672
/standard_name="M78946"
/note="matching EMBL:M78946; Identified using the e-PCR
software (G. Schuler)"
138800..138921
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/note="matching EMBL:H72023; Identified using the e-PCR
software (G. Schuler)"
161612..161756
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/note="matching EMBL:AA452257; Identified using the e-PCR
software (G. Schuler)"
194799..194898
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/note="matching EMBL:N91549; Identified using the e-PCR
software (G. Schuler)"

BASE COUNT 50873 a 45668 c 47123 g 52623 t
ORIGIN

Query Match 62.7%; Score 364.2; DB 10; Length 196287;
Best Local Similarity 90.1%; Pred. No. 2.9e-75;
Matches 390; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 atcccgacccagcctcaacccagacacacgcgctctagtggctgacttttagctat 60
Db 89821 ATGGCGACCCACCTCGGCCCCAGACACACGGGCTCTGTGGCAGACATTTGTAGTTAT 89880
QY 61 aggtcagcgagaaggggttatctgtgagctgggctggggaagggccagcccgacc 120
Db 89881 AAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 89940
QY 121 ccgctgcaacgaacgctgagctgagagagagttttagaccctttccgcgcacc 180
Db 89941 CCCTGCACCAAGCCATGCGGGAGCTGGAGATGAGTTCAGACCCCTTCCGGCGCACC 90000
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Qy 481 cgtctggggagggcaactgagtgagcacagtggtgacggggcccgctgacgctg 540
 Db 481 CGTCTGGGGAGGGAAGTGGGATCAGTGGAGGAGTGTGACGGGGCCGTGGCAGTG 540
 Qy 541 ggggcccctgtaactaggggccccttttttttctgtagcaagtg 581
 Db 541 GGGGCCCTGTGTAAGTGGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 6

D87461 LOCUS 3542 bp mRNA PRI 10-JUL-1997
 DEFINITION Human mRNA for KIAA0271 gene, complete cds.
 D87461
 ACCESSION D87461
 VERSION D87461.1 GI:1944417
 KEYWORDS KIAA0271
 SOURCE Homo sapiens male brain myoblast cell_line:KG-1 cDNA to mRNA,
 clone_lib:PSPORT 1 clone:HA6752.

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 3542)
 Nomura,N.

REFERENCE

AUTHORS Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
 TITLE Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobuo
 JOURNAL Nomura, Kazusa DNA Research Institute, Gene Structure 1: 1532-3
 Yana, Kizarazu, Chiba 292, Japan (E-mail:cdmainfo@kazusa.or.jp,
 URL:http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931)

REFERENCE

AUTHORS Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
 TITLE Prediction of the coding sequences of unidentified human genes. VI.
 The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
 analysis of cDNA clones from human cell line KG-1 and brain
 unpublished (1996)

JOURNAL

AUTHORS Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
 TITLE Prediction of the coding sequences of unidentified human genes. VI.
 The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
 analysis of cDNA clones from cell line KG-1 and brain

JOURNAL

MEDLINE DNA Res. 3 (5), 321-329 (1996)
 FEATURES Location/Qualifiers
 1..3542
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_line="KG-1"
 /cell_type="myoblast"
 /clone="HA6752"
 /clone_lib="PSPORT 1"
 /sex="male"
 /tissue_type="brain"
 177..758
 /gene="KIAA0271"
 177..758
 /gene="KIAA0271"
 /note="similar to human transforming protein bcl-2
 (A2428)"

gene

CDS 177..758

CDS

/codon_start=1
 /protein_id="BAA19666.1"
 /db_xref="GI:1944418"
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 AMRAGDFEERFRRTSDLAALHVTGPSAQORFTQVSDLEFQGNWGLVAFVFF
 GNAALCAESVKNEMEPVLGVQGVWVAYLETRLDWIHSSGWAETALYGDGALEAR
 RUREGNWASRVTLVTFGALVTVGVAFASK"
 BASE COUNT 804 a 817 c 1030 g 891 t

BASE COUNT 804 a 817 c 1030 g 891 t

Query Match

Best Local Similarity 86.5%; Score 502.6; DB 9; Length 3542;

Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1 atgcccagccccagcctcaacccccacacacacgcgcctagtggtgactttgttagctat 60
 Db 177 ATGGGACCCAGCCTCGGCCACAGACACAGGGCTCTGGTGGCAGACTTTGTAGGTAT 236
 Qy 61 aggtcagggcagaaggttatgtctgtgagctgggctggggaagccccagccgcgcag 120
 Db 237 AAGCTGAGGCAGAAAGGTTATGTCTGTGTGAGCTGCCGCCGGGAGGCCAGCAGCTGAC 296
 Qy 121 ccgctgcaaccaagccatcgggctgctgagacagagttgagacccttttccgcgcgacc 180
 Db 297 CCGCTGCAACCAAGCATCGGGCAGCTGGAGATGATGATTCGAGACCCCGCTTCCGCGCACC 356
 Qy 181 ttctctgacctggcgcctcagctacacgtgacccagctcagccagcaacgcttcacc 240
 Db 357 TTCCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACACGCTTACC 416
 Qy 241 caggtttccagcaactttttccaagggggccctaactggggccctctgttggcaattttt 300
 Db 417 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCCTTGTAGCCCTTCTT 476
 Qy 301 gtcttggggctgcccctgtgtgctgagagtgatcaacaagaataaggagcctttgtgga 360
 Db 477 GTCCTTGGGGCTGCACGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 536
 Qy 361 caagtccagagattgattcgctgacctaccctgagacacgtctgctgactggtatccacgc 420
 Db 537 CAAGTGACAGGAGTGTGATGGTGGCTTACTCTGAGAGACGGCTGGCTGATCCACAGC 596
 Qy 421 agtggcctggggcggacttcacagctctctatacggggacggggccctggagagcacgg 480
 Db 597 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGAGCGCGG 656
 Qy 481 cgtctgaggggagggcaactgggctgagtgagacacagtggtgacggggcgctggcactg 540
 Db 657 CGTCTGGCGGAGGGGAACCTGGGCATCAGTGAGGACAGCTGCTGACGGGGCGCGTGGC 716
 Qy 541 gggcccttgtaactgtaggggccttttttctagcaagtg 581
 Db 717 GGGCCCTTGCTAACTGTAGGGGCGCTTTTGTCTAGCAAGTG 757

RESULT 7

AR020780 LOCUS 579 bp DNA PAT 05-DEC-1998
 DEFINITION Sequence 2 from patent US 5789201.
 ACCESSION AR020780
 VERSION AR020780.1 GI:3975395
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 579)
 AUTHORS Guasteilla,J.
 TITLE Genes coding for bcl-y a bcl-2 homologue
 JOURNAL Patent: US 5789201-A 2 04-AUG-1998;
 FEATURES Location/Qualifiers
 source 1..579
 BASE COUNT 106 a 154 c 208 g 111 t
 ORIGIN

Query Match 85.6%; Score 497.4; DB 5; Length 579;

Best Local Similarity 91.2%; Pred. No. 7.5e-106; Mismatches 52; Conservative 0; Indels 0; Gaps 0;

Qy 1 atgcgccccagcctcaacccccacacacgcgcctagtggtgactttgttagctat 60
 Db 1 ATGGGACCCAGCCTCGGCCACAGACACAGGGCTCTGGTGGCAGACTTTGTAGGTAT 60
 Qy 61 aggtcagggcagaaggttatgtctgtgagctgggctggggaagccccagccgcgcag 120
 Db 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGAGCTGCCGCCGGGAGGCCAGCAGCTGAC 120


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RESULT 1
MMU59746      582 bp      mRNA      29-SEP-1996
LOCUS      Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
DEFINITION
VERSION      U59746.1 GI:1572494
KEYWORDS
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 582)
AUTHORS      Gibson,L., Holmgren,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)
MEDLINE      96358615
REFERENCE
2 (bases 1 to 582)
AUTHORS      Gibson,L., Holmgren,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
Cory,S.
Direct Submission
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia
LOCATION/Qualifiers
1. 582
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1. 582
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1. 582
/gene="bcl-w"
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/codon_start=1
/product="Bcl-w"
/protein_id="AAB09056.1"
/db_xref="GI:1572495"
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GAALCAENKPELVQVQDMVAYLETRLADWIHSSGGWAEFTALYGDGALEAR
RLREGNWSVRYTLTGVALGALVTVGAFASK"
BASE COUNT      107 a 158 c 200 g 117 t
ORIGIN

Query Match      96.4%; Score 560.2; DB 12; Length 582;
Best Local Similarity 97.8%; Pred. No. 2e-120;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Db 1 ATGGGACCCAGCCCTCAACCCACACACGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 aggcagagcagaagggttatgtctgtgagctggcctggcgggaagccagcccgac 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 AAGCTGAGCAGAGGGTTATGCTGTGGAGCTGGCCCTGGGGAAGCCAGCCGCCGAC 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 121 ccgtgcaccagccatcgccgctgctgagacagagttgagaccgtttccgcgcacc 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 CCGCTGCACCAAGCCATCGGGGCTGCTGGAGACGAGTTTGAGACCCGCTTCGCCGCC 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 181 ttcttgacctggcctcagctacagctgacccagcctcagccagcagccttcacc 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCACGACGCTTACC 240
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Qy 241 cagggtttccgacgaactttccaaaggggcccctaacctggggccgtcttctgtgacatttt 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 CAGGTTTCGACGAACTTTCCAAAGGGGCCCTTAACGGGGCCGCTCTGTGGCACTTT 300
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Qy 301 gtctttggggtgcctgtgtgctgagagtgctcaacaaagaatggagcctttggtgga 360
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Db 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGGGA 360
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Qy 361 caagtcacagattgattgctgacctacctgagacacacgtctgctgactgactgacacgc 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 361 CAAGTGCAGGATTGGATTGGTGGCCCTACCTCGGAGACACAGTCTGGCTGACTGGATCCACAGC 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 421 agtgccgctggcggacttcacagctctatcacgggggacggccctggagacgcacgg 480
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Db 421 AGTGGGGCTGGCGGAGTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGCAGG 480
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Qy 481 cgtctgcggaggggcaactggcctgagtgagcacagtggtgacggggggcggcgtggcactg 540
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Qy 541 gggggcctgttaactgtaggcctcttttcttagcaagtg 581
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Db 541 GGGGCCCTGTAACGTAGTAGGGCCCTTTTGTCTACCAAGTG 581
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RESULT 2
AF030769      3476 bp      mRNA      16-NOV-1997
LOCUS      Mus musculus Bcl-w (Bcl-w) mRNA, complete cds.
DEFINITION
ACCESSION      AF030769
VERSION      AF030769.1 GI:2623249
KEYWORDS
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 3476)
AUTHORS      Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and
MacGregor,G.R.
Bcl-w is required for testis homeostasis
Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 3476)
AUTHORS      Ross,A.J. and MacGregor,G.R.
Direct Submission
Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
University, 1462 Clifton Road, Atlanta, GA 30322, USA.
LOCATION/Qualifiers
1. 3476
/organism="Mus musculus"
/strain="C57BL/10J"
/db_xref="taxon:10090"
/chromosome="14"
/map="19.5 cm"
1. 3476
/gene="Bcl-w"
1. 82
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83. 170
/gene="Bcl-w"
/number=2
171. 610
/gene="Bcl-w"
/number=3
179. 760
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AMRAGDEFERFRFTSDIAQLHVTGPSAQORFQVSDLELFGQPNWGRVLAFFVF
GAALCAENKPELVQVQDMVAYLETRLADWIHSSGGWAEFTALYGDGALEAR
RLREGNWSVRYTLTGVALGALVTVGAFASK"
611. 3476
/gene="Bcl-w"
/number=4
3356. 3364
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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-636.198 Million cell updates/sec

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Perfect score: 581
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 882769 seqs, -486395729 residues
Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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18: em_hum1.*
19: em_hum2.*
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30: em_un.*
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33: gb_htg2.*
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36: em_bal.*
37: em_ba2.*
38: em_hum3.*
39: em_hum4.*
40: gb_pr4.*
41: gb_htg3.*
42: gb_htg4.*
43: gb_htg5.*
44: gb_htg6.*

45: gb_htg7.*
46: em_htg1.*
47: em_htg2.*
48: em_htg3.*
49: em_hum5.*
50: gb_pl3.*
51: gb_pr5.*
52: gb_htg8.*
53: gb_htg9.*
54: gb_htg10.*
55: gb_htg11.*
56: gb_htg12.*
57: gb_htg13.*
58: gb_htg14.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	560.2	96.4	582	12	MMU59746	U59746 Mus musculu
2	560.2	96.4	3476	12	AF030769	AF030769 Mus muscu
3	544.2	93.7	582	12	AF096291	AF096291 Rattus no
4	540.6	93.0	579	5	AR020779	AR020779 Sequence
5	505.8	87.1	582	10	HS059747	U59747 Human Bcl-w
6	502.6	86.5	3542	9	D87461	D87461 Human mRNA
7	497.4	85.6	579	5	AR020780	AR020780 Sequence
8	364.2	62.7	196287	10	CNS0000B	AL049829 Human chr
9	233.8	40.2	749	4	XLRL	X82462 X.laavis R1
10	138.2	23.8	1184	4	GG026645	U26645 Gallus gall
11	134.6	23.2	926	5	AR054021	AR054021 Sequence
12	134.6	23.2	926	5	I52011	I52011 Sequence 5
13	134.6	23.2	926	9	HSBCLXL	Z23115 H.sapiens b
14	134.2	23.1	720	3	AF216205	AF216205 Sus scrof
15	134.2	23.1	752	3	SSJ001203	AJ001203 Sus scrof
16	131.8	22.7	764	12	RNU10579	U10579 Rattus norv
17	131.8	22.7	1742	12	RNU72350	U72350 Rattus norv
18	131.8	22.7	2232	12	RNCBLXLS	X82537 R.norvegicu
19	127	21.9	708	12	RNU34964	U34964 Rattus norv
20	127	21.9	726	12	RNU34963	U34963 Rattus norv
21	127	21.9	726	12	S76513	S76513 bcl-x-apopt
22	126.8	21.8	723	10	HS072398	U72398 Human Bcl-x
23	126.8	21.8	74673	42	AC016218	AC016218 Homo sapi
24	126.8	21.8	151029	33	HSJ7857M17	AL117381 Homo sapi
25	126.6	21.8	687	3	BT092434	U92434 Bos taurus
26	126.4	21.8	699	12	MMBCLXL	X83574 M.musculus
27	126.4	21.8	702	12	MMU10101	U10101 Mus musculu
28	126.4	21.8	979	12	MUSBCLX	L35049 Mus musculu
29	126.4	21.8	1466	12	MMU51278	U51278 Mus musculu
30	126.4	21.8	5771	14	AF060226	AF060226 Eukaryoti
31	125	21.5	717	5	AR052622	AR052622 Sequence
32	125	21.5	765	5	A76121	A76121 Sequence 1
33	125	21.5	5086	5	AR052621	AR052621 Sequence
34	125	21.5	5086	5	AR054008	AR054008 Sequence
35	125	21.5	5086	9	HUMBCL2A	M13994 Human B-cel
36	125	21.5	5105	5	I08038	I08038 Sequence 1
37	125	21.5	6030	9	HUMBCL2C	M14745 Human bcl-2
38	123.8	21.3	1179	12	RATBCL2A	L14680 Rattus norv
39	123.4	21.2	760	5	AR021160	AR021160 Sequence
40	123.4	21.2	1846	5	AR054009	AR054009 Sequence
41	123.4	21.2	1846	9	HSECL2IG	X06487 H.sapiens m
42	120.2	20.7	1274	4	GGBCLX	Z23110 G.gallus bc
43	120.2	20.7	1274	5	AR054019	AR054019 Sequence
44	120.2	20.7	1303	5	I52010	I52010 Sequence 1
45	120.2	20.7	1748	12	RNU72349	U72349 Rattus norv

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DR EMBL; U16812; AAA74467.1; -.
DR HSP; Q16611; 1BXL.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PFAW; PF00452; Bcl-2; 1.
KW Apoptosis; Transmembrane.
FT DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 211 AA; 23411 MW; 703875EC4DCCC1D3 CRC64;

Query Match 16.9%; Score 234; DB 1; Length 211;
Best Local Similarity 31.5%; Pred.No. 2.28e-26;
Matches 34; Conservative 28; Mismatches 44; Indels 2; Gaps 2;

Db 82 GDDINRRYDSEFTQMLQHOPTAENAYEFTKIASLPSGINSGRVVALIGFSYRLALH 141

QY 50 GDEFETRFRRTESDLAAQLHVTGPSAQQRFTQVSDLEFGGPNMGRVAVFFVGAALCAE 109

Db 142 IYQRLTGLGQVTRFVYDFMLHHCIARWIAQORGWVAALNL-GNGPI 188

QY 110 SYNKEMLVGVQDQWIVAY-LETRLADWIHSSGGWADFTALYGDGAL 156

Search completed: Fri Jun 23 14:18:55 2000
Job time : 11 secs.

RX MEDLINE; 92096610.
 RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
 RT "Frequent incidence of somatic mutations in translocated BCL2
 RT oncogenes of non-Hodgkin's lymphomas.";
 RL Blood 79:229-237(1992).
 RN [6]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE; 91066924.
 RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
 RT programmed cell death.";
 RL Nature 348:334-336(1990).
 RN [7]
 RP MUTAGENESIS.
 RX MEDLINE; 94239528.
 RA Yin X.-M., Oltvai Z.N., Korsmeyer J.;
 RT "Bhl and Bh2 domains of Bcl-2 are required for inhibition of
 RT apoptosis and heterodimerization with Bax.";
 RL Nature 369:321-323(1994).
 CC -!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
 CC ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
 CC VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
 CC BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
 CC ANTI-OXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
 CC GENERATION SUCH AS MITOCHONDRIA.
 CC -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
 CC BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX
 CC REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-
 CC APOPTOTIC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
 CC WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
 CC -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA. ARE
 CC PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
 CC DIFFER AT THEIR C-TERMINAL ENDS.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
 CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
 CC FUNCTION.
 CC -!- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
 CC II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
 CC T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
 CC REGIONS.
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC EMBL; M13994; AAA51813.1; ALT_SEQ.
 CC EMBL; M13995; AAA51814.1; ALT_SEQ.
 CC EMBL; M1745; AAA35591.1; -.
 CC EMBL; X06487; CAA29778.1; -.
 CC EMBL; S72602; AAD14111.1; ALT_SEQ.
 CC PIR; A29409; TVHUA1.
 CC PIR; B29409; TVHUB1.
 CC PIR; A24428; TVHUBC.
 CC PIR; C37332; C37332.
 CC PIR; D37332; D37332.
 CC HSP; P53563; IAF3.
 CC MIM; 151430; -.
 CC PROSITE; PS50062; BCL2_FAMILY; 1.
 CC PROSITE; PS01080; BH1; 1.
 CC PROSITE; PS01258; BH2; 1.
 CC PROSITE; PS01259; BH3; 1.
 CC PROSITE; PS01260; BH4_1; 1.

DR PROSITE; PS50063; BH4_2; 1.
 KW PF00452; Bcl-2; 1.
 KW Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
 KW Mitochondrion; Chromosomal translocation; Polymorphism;
 KW Disease mutation.
 FT DOMAIN 10 30 BH4.
 FT DOMAIN 93 107 BH3.
 FT DOMAIN 136 155 BH1.
 FT DOMAIN 187 202 BH2.
 FT TRANSMEM 212 233 POTENTIAL.
 FT VARSPPLIC 196 239 DAELYGFMRPLDFSWLSKLTLLSLALVGACITLGAYL
 FT MUTAGEN 145 145 GHK -> VGASGDVS (IN ISOFORM BCL-2-BETA).
 FT MUTAGEN 188 188 G->A: NO HETERODIMERIZATION WITH BAX, AND
 FT MUTAGEN 188 188 LOSS OF ANTI-APOPTOTIC ACTIVITY.
 FT VARIANT 7 7 W->A: NO HETERODIMERIZATION WITH BAX, AND
 FT VARIANT 59 59 LOSS OF ANTI-APOPTOTIC ACTIVITY.
 FT VARIANT 59 59 T -> S.
 FT VARIANT 59 59 /FTID-VAR_000827.
 FT VARIANT 59 59 P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
 FT VARIANT 93 93 MUTATION).
 FT VARIANT 93 93 V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
 FT VARIANT 93 93 /FTID-VAR_000828.
 FT VARIANT 93 93 V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
 FT VARIANT 93 93 MUTATION).
 FT CONFLICT 48 48 I -> F (IN REF. 4).
 FT CONFLICT 59 59 P -> T (IN REF. 3).
 FT CONFLICT 117 117 S -> R (IN REF. 3).
 FT CONFLICT 129 129 R -> C (IN REF. 4).
 SQ SEQUENCE 239 AA; 26266 MW; 3C49F2B714DC9CCB CRC64;
 Query Match 40.1%; Score 556; DB 1; Length 239;
 Best Local Similarity 43.3%; Pred. No. 1.27e-98;
 Matches 71; Conservative 46; Mismatches 41; Indels 6; Gaps 4;
 Db 81 AAGPALSPVPVHLTRQAGDDFSRRYRDFRDMSSQLHLTFTTARGRATVVEELFRD 140
 QY 30 GAGPGEPAADPLHQAMRAAGDEFRTFRFSDLAQLHVTGSAQOQRTQVSDLEFQG 89
 Db 141 GVNNGRIVAFEFGGVNCVSVNRENSPLVDNTALMTVLRHLHTWIDNGSGDAFVE 200
 QY 90 GPNMGRULVAFVFGALCAESVNKEMPLVGQVQDVLVAYLTRLADWTHSSGGWADFTA 149
 Db 201 LYGP-SM---RPLDFSWLSKLTLLSLAL-VGACITLGAYLGHK 239
 QY 150 LYGDGALEDARRLRREGNW-AVSVTVTGAVALGALVTGAFVASK 192
 RESULT 12
 ID BCL2_MOUSE STANDARD; PRT; 236 AA.
 AC P10417; P10418;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE APOPTOSIS REGULATOR BCL-2.
 GN BCL2 OR BCL-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=LIVER;
 RX MEDLINE; 87187643.
 RA Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;
 RT "Molecular analysis of mbcl-2: structure and expression of the murine
 RT gene homologous to the human gene involved in follicular lymphoma.";
 RL Cell 49:455-463(1987).
 RN [2]
 RP REVISIONS TO 221-222.
 RX MEDLINE; 92375724.
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
 RT "Isolation and characterization of the chicken bcl-2 gene: expression
 RT in a variety of tissues including lymphoid and neuronal organs in
 RT adult and embryo.";

RC TISSUE-BRAIN;
RX MEDLINE; 94193015.
RA Sato T., Irie S., Krajewski S., Reed J.C.;
RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL Gene 140:291-292(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
RX MEDLINE; 95129487.
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
cell apoptosis is associated with decreased bax and constitutive
bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
RN [3]
RP SEQUENCE OF 19-172 FROM N.A.
RX MEDLINE; 95059917.
RA Castren E., Onga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
RL Lindholm D.;
RT "bcl-2 messenger RNA is localized in neurons of the developing and
adult rat brain.";
RL Neuroscience 61:165-177(1994).
CC -1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
GENERATION SUCH AS MITOCHONDRIA.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
BAX PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX
REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-
APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
DIFFER AT THEIR C-TERMINAL ENDS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES, WITH
HIGHEST LEVELS IN REPRODUCTIVE TISSUES. IN THE ADULT BRAIN,
EXPRESSION IS LOCALIZED IN MITRAL CELLS OF THE OLFACTORY BULB,
GRANULE AND PYRAMIDAL NEURONS OF HIPPOCAMPUS, PONTINE NUCLEI,
CEREBELLAR GRANULE NEURONS, AND IN EPENDYMAL CELLS. IN PRENATAL
BRAIN, EXPRESSION IS HIGHER AND LOCALIZED IN THE NEUROEPITHELIUM
AND IN THE CORTICAL PLATE.
CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
FUNCTION.
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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DR EMBL; L14680; AAA53662.1; -;
DR EMBL; U34964; AAA77687.1; -;
DR EMBL; S74122; CAB33200.1; -;
DR HSSP; P53563; 1AF3.
DR PROSITE; P550062; BCL2_FAMILY; 1.
DR PROSITE; P501080; BH1; 1.
DR PROSITE; P501258; BH2; 1.
DR PROSITE; P501259; BH3; 1.
DR PROSITE; P501260; BH4_1; 1.
DR PROSITE; P550063; BH4_2; 1.
DR PFWA; PF00452; Bcl-2; 1.

KW Apoptosis; Alternative splicing; Transmembrane; Mitochondrion.
FT DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT CONFLICT 42 42 A -> R (IN REF. 2).
FT CONFLICT 157 157 E -> G (IN REF. 1).
FT CONFLICT 164 164 S -> Y (IN REF. 2).
FT CONFLICT 212 212 L -> Q (IN REF. 2).
SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;
Query Match 40.1%; Score 556; DB 1; Length 236;
Best Local Similarity 43.4%; Pred. No. 1.27e-98;
Matches 72; Conservative 45; Mismatches 43; Indels 6; Gaps 4;
Db 76 VANAGPALSPPVPHVHLTRAGDDFSRRYRRDFAEMSSQLHLTPFARGRAFTVVEELF 135
QY 28 VCGAGPGEPAADPLHQAMRAAGDEFETFRFTFSLAAQLHVTGSAQOQRTQVSDLELF 87
Db 136 RDGVNMGRIYAFTEFGVCMVESVNRMSPLVDNIALMWTYLNRLHLTWIODNGGWDAF 195
QY 88 QGGPNMGRLVAFVFGAALCAESVKNEMELVQGVQVDWIVAYLETRADWIHSSGGWADF 147
Db 196 VEYGP-SM---RPLDFSWLSKLTLSIAL-VGACITLGAYLGHK 236
QY 148 TALYDGALEDARRLRREGNW-AVSTVTGTGVALGALVTVGAFPAK 192
RESULT 11
ID BCL2_HUMAN STANDARD; PRT; 239 AA.
AC P10415; P10416; Q16197; Q13842;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE APOPTOSIS REGULATOR BCL-2.
GN BCL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86259760.
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of
bcl-2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE; 92375724.
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
in a variety of tissues including lymphoid and neuronal organs in
adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87002488.
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
2/immunoglobulin transcript resulting from the t(14;18)
translocation.";
RL Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88196071.
RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation
of the Bcl-2-Ig fusion gene in lymphoma.";
RL EMBO J. 7:123-131(1988).
RN [5]
RP SEQUENCE OF 1-131 FROM N.A., AND VARIANTS NON-HODGKINS-LYMPHOMA.

QY 101 VEGAALCAESVKNEMPLVGQVQWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160
Db 205 KGOERENWELTGMTVAGVLLGSL 229
QY 161 RLREG-N-WAVSTV-VTGAVALGAL 182

RESULT 7
ID BCLX_CHICK STANDARD; PRT; 229 AA.
AC Q07816; Q98908;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE APOPTOSIS REGULATOR BCL-X.
GN BCL2L1 OR BCLX OR BCL-X.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
CC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
RX MEDLINE; 93364977.
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death.";
RL Cell 74:597-608(1993).
[2]
RN SEQUENCE FROM N.A. (SHORT FORM).
RP MEDLINE; 93364977.
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death.";
RL Cell 74:597-608(1993).
[2]
RN SEQUENCE FROM N.A. (LONG FORM).
RC STRAIN=HUBBARD WHITE MOUNTAIN; TISSUE=TESTIS;
RX MEDLINE; 97264485.
RA Villagrasa X., Mezquita C., Mezquita J.;
RT "Differential expression of bcl-2 and bcl-x during chicken
RT spermatogenesis.";
RL Mol. Reprod. Dev. 47:26-29(1997).
CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT
CC ISOFORM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
CC DEVELOPMENT.
CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 4 (BH4).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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CC EMBL; 223110; CAA80657.1; -.
CC EMBL; U26645; AAB07677.1; -.
CC PIR; A47537; A47537.
CC HSP; P53563.1AF3.
CC PROSITE; PS50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01260; BH4_1; 1.
CC PROSITE; PS50063; BH4_2; 1.
CC PFAM; PF00452; Bcl-2; 1.
CC Apoptosis; Transmembrane; Alternative splicing.

FT DOMAIN 4 24 BH4.
FT DOMAIN 82 96 BH3.
FT DOMAIN 125 144 BH1.
FT DOMAIN 176 191 BH2.
FT TRANSMEM 206 223 POTENTIAL.
FT VARSPPLIC 185 229 ERFVDLYGNNAAEERKGOETFNKWLKTGATVAGVLLGSL
SQ SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0B9DA CRC64;
Query Match 44.7%; Score 620; DB 1; Length 229;
Best Local Similarity 51.7%; Pred. No. 1.09e-113;
Matches 77; Conservative 33; Mismatches 36; Indels 3; Gaps 3;
Db 79 ASDVROALRDAGDEFFELRYRRAFSDLTSLHITPGTAYQSFQVYVNFPHDGVNMGRIYA 138
QY 39 ADPLHQAMRAAGDEFFETFRRTFSDLAQLHVTGPSAQORFTQVSDQLFQGGPNMGRIVA 98
Db 139 FFSFGALCVESVDKMRVLGRIVSWMTYTLTHLDPWIQENGWGERFVDLYGNNAAE 198
QY 99 FFVFGAALCAESVKNEMPLVGQVQWIVAYLETRLADWIHSSGGWADFTALYGDGALED 158
Db 199 LRKGOETFNKWLKTGATVAGVLLGSL 227
QY 159 ARRLREG-N-WAVS-TVVTGAVALGALVT 184

RESULT 8
ID BCLX_PIG STANDARD; PRT; 233 AA.
AC Q07737;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE APOPTOSIS REGULATOR BCL-X.
GN BCL2L1 OR BCL2L OR BCLX.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
[1]
RN SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT AND
CC THE BETA ISOFORMS PROMOTE APOPTOSIS.
CC -1- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
CC BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 4 (BH4).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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CC EMBL; AJ001203; CAA04597.1; -.
CC PROSITE; PS50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.

SQ SEQUENCE 233 AA; 26049 MW; E09D3CDD851AE9BE CRC64;
Query Match 44.9%; Score 623; DB 1; Length 233;
Best Local Similarity 52.4%; Pred. No. 2.13e-114;
Matches 76; Conservative 34; Mismatches 32; Indels 3; Gaps 3;
Db 85 AVKQALREAGDEFEELRYRAFSDLTSLQHTPGTAYQSFQVNVNLFPRDGVNNGRIVAEF 144
QY 41 PLHQANRAAGDEFEFRFRFTSDLAQJLHVTPGSAQORFTQVSEDLFCGGPNWGLVAF 100
Db 145 SFGGALCVESVDKEMQVLSRIAAMATYLNHLEPWIQENGWDTFVELYGNNAAESR 204
QY 101 VEGALCAESYNKEMPLVGQVDWIVAYLETRLADMTIHSSGGWADFTALYGDGALEDAR 160
Db 205 KQGRFNWFLTGMTVAGVLLGSL 229
QY 161 RLREG-N-WAVSTV-VTGAVALGAL 182
RESULT 6
ID BCLX_MOUSE STANDARD; PRT; 233 AA.
AC Q64373; Q60657; Q60658; Q61338;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE APOPTOSIS REGULATOR BCL-X.
GN BCL2L1 OR BCL2L OR BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=244B;
RA Kanesaki H., Michaud G.Y., Takatsu K., Okuma M.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
RC STRAIN=C57BL/6; TISSUE=BRAIN;
RX MEDLINE; 95331139.
RA Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L., Boise L.H.,
RT Thompson C.B., Nunez G.;
RT "bcl-XL is the major bcl-x mRNA form expressed during murine
RT development and its product localizes to mitochondria."
RL Development 120:3033-3042(1994).
RN [3]
RP SEQUENCE FROM N.A. (X(L); X(S) AND X(DELTA-TM) ISOFORMS).
RC TISSUE=PRE-B CELL;
RX MEDLINE; 95052604.
RA Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
RT "Cloning and molecular characterization of mouse bcl-x in B and T
RT lymphocytes."
RL J. Immunol. 153:4388-4398(1994).
RN [4]
RP SEQUENCE FROM N.A. (BETA ISOFORM).
RC STRAIN=C57BL/6 X CBA; TISSUE=THYMUS;
RX MEDLINE; 98051053.
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
RT apoptosis in T cells."
RL Immunology 7:629-639(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97289584.
RA Grillo D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
RA Ohta S., Seldin M.F., Nunez G.;
RT "Genomic organization, promoter region analysis, and chromosome
RT localization of the mouse bcl-x gene."
RL J. Immunol. 158:4750-4757(1997)
CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC FORM AND THE DELTA-TM FORM DISPLAY CELL DEATH REPRESSOR ACTIVITY,
CC WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH

CC BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
CC -1- ALTERNATIVE PRODUCTS: FOUR ISOFORMS, BCX-X(L) (SHOWN HERE), BCL-
CC X(S), BCL-X-BETA AND BCL-X(DELTA-TM), ARE DERIVED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE
CC BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-
CC TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
CC ACTIVATED.
CC -1- DEVELOPMENTAL STAGE: BCL-X(BETA) IS EXPRESSED IN BOTH EMBRYONAL AND
CC POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN
CC POSTNATAL TISSUES.
CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC
CC EMBL; X83574; CAA58557.1; -
CC EMBL; L35049; AA51039.1; -
CC EMBL; L35048; AA51040.1; -
CC EMBL; U10102; AA82174.1; -
CC EMBL; U10101; AA82173.1; -
CC EMBL; U10100; AA82172.1; -
CC EMBL; U51279; AAC53460.1; -
CC EMBL; U78031; AAB96881.1; -
CC EMBL; U78030; AAB96881.1; JOINED.
CC HSSP; P53563; IAF3.
CC MGD; MGI:88139; BCL2L.
CC PROSITE; P50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01260; BH4_1; 1.
CC PROSITE; P50063; BH4_2; 1.
CC PFAM; PF00452; Bcl-2; 1.
CC Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
FT VARSPPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).
FT VARSPPLIC 189 233 DTFVDLYGNNAESRKQGRFNWFLTGMTVAGVLLGSL
FT BCL-X-BETA).
FT VARSPPLIC 194 233 LYGNNAEAESRKQGRFNWFLTGMTVAGVLLGSLFSRK
FT -> GHDCGWCWSAGLTLQSEVTRH (IN ISOFORM BCL-
FT X(DELTA-TM)).
SQ SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072E CRC64;
Query Match 44.9%; Score 623; DB 1; Length 233;
Best Local Similarity 52.4%; Pred. No. 2.13e-114;
Matches 76; Conservative 34; Mismatches 32; Indels 3; Gaps 3;
Db 85 AVKQALREAGDEFEELRYRAFSDLTSLQHTPGTAYQSFQVNVNLFPRDGVNNGRIVAEF 144
QY 41 PLHQANRAAGDEFEFRFRFTSDLAQJLHVTPGSAQORFTQVSEDLFCGGPNWGLVAF 100
Db 145 SFGGALCVESVDKEMQVLSRIAAMATYLNHLEPWIQENGWDTFVELYGNNAEAESR 204

FT CONFLICT 81 81 I -> L (IN REF. 4).
FT CONFLICT 119 119 A -> V (IN REF. 4).
FT CONFLICT 143 144 FF -> SS (IN REF. 4).
FT CONFLICT 199 199 A -> T (IN REF. 4).
FT CONFLICT 201 201 A -> P (IN REF. 4).
SQ SEQUENCE 233 AA; 26158 MW; 2B62B6C63864BC8F CRC64;

Query Match 44.9%; Score 623; DB 1; Length 233;
Best Local Similarity 52.4%; Pred. No. 2.13e-114;
Matches 76; Conservative 34; Mismatches 32; Indels 3; Gaps 3;

Db 85 AVKQALRAGDEFEYRARRSRLTSQHIPTGAYQSFQVNELEFRDGVNNGRIYVAF 144
QY 41 PLHQAMRAAGDEFEYRARRSRLTSQHIPTGAYQSFQVNELEFRDGVNNGRIYVAF 100

Db 145 SPGGALCVESVDKQVLSRIASWMTYLNHLEPWIQENGWDTFVDLYGNNAAESR 204
QY 101 VEGAALCAESNNKEPLVGQVQDMIVAYLETRUADWTHSSGGWADFTALYGDGALEDAR 160

Db 205 KGQERFNWFLTGMTVAGVLLGSL 229
QY 161 RLREG-N-WAVSTV-VTGAVALGAL 192

RESULT 5
ID BCLX_HUMAN STANDARD; PRT; 233 AA.
AC Q07817; Q92976;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE APOPTOSIS REGULATOR BCL-X.
GN BCL2L1 OR BCL2L OR BCLX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
RX MEDLINE; 93364977.
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
of apoptotic cell death.";
RL Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (BETA ISOFORM).
RA Inohara N., Ohta S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX MEDLINE; 95372373.
RA Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA Korsmeyer S.J.;
RT "Multiple Bcl-2 family members demonstrate selective dimerizations
with Bax.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN [4]
RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX MEDLINE; 96170038.
RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA Korsmeyer S.J.;
RT "Bax-independent inhibition of apoptosis by Bcl-XL.";
RL Nature 379:554-556(1996).
RN [5]
RP STRUCTURE BY NMR OF 1-209.
RX MEDLINE; 97172562.
RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA Thompson C.B., Pesik S.W.;
RT "Structure of Bcl-XL-Bak peptide complex: recognition between
regulators of apoptosis.";
RL Science 275:983-986(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.

RX MEDLINE; 96256675.
RA Yoon H.S., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA Ng S.L., Pesik S.W.;
RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed
cell death.";
RL Nature 381:335-341(1996).
CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
ISOFORM PROMOTES APOPTOSIS.
CC -1- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
ENVELOPE (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS, BCL-X(L) (SHOWN HERE),
BCL-X(S) AND BCL-X(BETA), ARE DERIVED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
APOPTOTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC EMBL; 2231116; CAA80662.1; -
CC EMBL; 2231115; CAA80661.1; -
CC EMBL; U723398; AAB17334.1; -
CC FDB; 1BXL; 29-OCT-97.
CC FDB; 1LXL; 21-APR-97.
CC FDB; 1MAZ; 21-APR-97.
CC MIM; 600039; -
CC PROSITE; PS50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01260; BH4_1; 1.
CC PROSITE; PS50063; BH4_2; 1.
CC PFAM; PF00452; Bcl-2; 1.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW 3d-structure.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
FT VARSPPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).
FT VARSPPLIC 189 233 DTFVELYGNNAAESRKGQERFNWFLTGMTVAGVLLGSL
FT FSRK -> VRTKPLVCPFSLAGQSRPTALLLYLFLLCWVI
FT VGDVDS (IN ISOFORM BCL-X(BETA)).
FT FRD->VRA: NO HETERODIMERIZATION WITH BAX.
FT VNW->AIL: LOSS OF ANTI-APOPTOTIC
FT ACTIVITY.
FT GRI->ELN: LOSS OF ANTI-APOPTOTIC
FT ACTIVITY.
FT G->A: NO HETERODIMERIZATION WITH BAX.
FT G->E: NO HETERODIMERIZATION WITH BAX.
FT WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
BY ABOUT HALF.
FT G -> A (IN CAA80661).
FT CONFLICT 70 70


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DR EMBL; AF030769; AAB86430.1; -.
DR HSP; P53563; 1AF3.
DR MGI; 108052; BCL2L2.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH4_2; 1.
DR PFAM; PF00452; Bcl-2; 1.
DR Apoptosis.
KW Apoptosis.
FT DOMAIN 9 29 BH4.
FT DOMAIN 85 104 BH1.
FT DOMAIN 136 151 BH2.
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DEB4 CRC64;

Query Match 97.0%; Score 1345; DB 1; Length 193;
Best Local Similarity 95.9%; Pred. No. 1.76e-289;
Matches 185; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

Db 1 MATPASTPDTRALVADFGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFFETFRRT 60
QY 1 MPTPASTPDTRALVADFGYRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFFETFRRT 60
Db 61 FSDLAALHVTGSAQORFTQVSDLELFGGPNWGRVLAFFVFGAALCAESVKNEMEPLVG 120
QY 61 FSDLAALHVTGSAQORFTQVSDLELFGGPNWGRVLAFFVFGAALCAESVKNEMEPLVG 120
Db 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYDGDGALEARRLRREGNWSVTVLTGAVAL 180
QY 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYDGDGALEARRLRREGNWSVTVLTGAVAL 179
Db 181 GALVTGGAFFASK 193
QY 180 GALVTGGAFFASK 192

RESULT 2
ID BCLW_HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE APOPTOSIS REGULATOR BCL-W (KIAA0271).
GN BCL2L2 OR BCLW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96359615.
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RA "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97191544.
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RA "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
CC -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC AND SALIVARY GLAND.
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION.
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
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CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 4 (BH4).
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC
CC EMBL; U59747; AAB09055.1; -.
CC EMBL; D87461; BAA19666.1; -.
CC HSP; P53563; 1AF3.
CC MIM; 601931; -.
CC PROSITE; PS50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01260; BH4_1; 1.
CC PROSITE; PS01260; BH4_2; 1.
CC PFAM; PF00452; Bcl-2; 1.
CC Apoptosis.
KW Apoptosis.
FT DOMAIN 9 29 BH4.
FT DOMAIN 85 104 BH1.
FT DOMAIN 136 151 BH2.
SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

Query Match 96.8%; Score 1341; DB 1; Length 193;
Best Local Similarity 94.8%; Pred. No. 1.70e-288;
Matches 183; Conservative 8; Mismatches 1; Indels 1; Gaps 1;

Db 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFFETFRRT 60
QY 1 MPTPASTPDTRALVADFGYRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFFETFRRT 60
Db 61 FSDLAALHVTGSAQORFTQVSDLELFGGPNWGRVLAFFVFGAALCAESVKNEMEPLVG 120
QY 61 FSDLAALHVTGSAQORFTQVSDLELFGGPNWGRVLAFFVFGAALCAESVKNEMEPLVG 120
Db 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYDGDGALEARRLRREGNWSVTVLTGAVAL 180
QY 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYDGDGALEARRLRREGNWSVTVLTGAVAL 179
Db 181 GALVTGGAFFASK 193
QY 180 GALVTGGAFFASK 192

RESULT 3
ID ARL_XENLA STANDARD; PRT; 228 AA.
AC Q91827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE APOPTOSIS REGULATOR R1 (XR1) (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96359615.
RA Cruz-Reyes J., Tata J.R.;
RA "Cloning, characterization and expression of two Xenopus bcl-2-like
RT cell-survival genes.";
RL Gene 158:171-179(1995).
CC -!- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
CC -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHIC TO POST-METAMORPHIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
```

MAISREH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Jun 23 14:18:44 2000; MasPar time 8.06 Seconds
Tabular output not generated. 725.519 Million cell updates/sec

Title: >US-09-155-327B-9
Description: (1-192) from US09155327B.pep
Perfect Score: 1386
Sequence: 1 MPTPASTPDTRALVADFGV.....VTGVALGALVTYGAFFASK 192

Scoring table: PAM 150
Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 45.917; Variance 78.366; scale 0.586

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1345	97.0	193	1	BCLW_MOUSE APOPTOSIS REGULATOR BC	1.76e-289
2	1341	96.8	193	1	BCLW_HUMAN APOPTOSIS REGULATOR BC	1.70e-288
3	900	64.9	228	1	ARL_XENLA APOPTOSIS REGULATOR R1	9.34e-181
4	623	44.9	233	1	BCLX_RAT APOPTOSIS REGULATOR BC	2.13e-114
5	623	44.9	233	1	BCLX_HUMAN APOPTOSIS REGULATOR BC	2.13e-114
6	623	44.9	233	1	BCLX_MOUSE APOPTOSIS REGULATOR BC	2.13e-114
7	620	44.7	229	1	BCLX_CHICK APOPTOSIS REGULATOR BC	1.09e-113
8	613	44.2	233	1	BCLX_PIG APOPTOSIS REGULATOR BC	4.92e-112
9	561	40.5	233	1	BCL2_CHICK APOPTOSIS REGULATOR BC	8.52e-100
10	556	40.1	236	1	BCL2_RAT APOPTOSIS REGULATOR BC	1.27e-98
11	556	40.1	239	1	BCL2_HUMAN APOPTOSIS REGULATOR BC	1.27e-98
12	554	40.0	236	1	BCL1_MOUSE APOPTOSIS REGULATOR BC	3.72e-98
13	546	39.4	204	1	ARL1_XENLA APOPTOSIS REGULATOR R1	2.78e-96
14	235	17.0	211	1	BAK_HUMAN BCL-2 HOMOLOGOUS ANTAG	1.42e-26
15	234	16.9	211	1	BAK2_HUMAN BCL-2 HOMOLOGOUS ANTAG	2.28e-26
16	229	16.5	192	1	BAXA_RAT APOPTOSIS REGULATOR BA	2.45e-25
17	229	16.5	192	1	BAXA_MOUSE APOPTOSIS REGULATOR BA	2.45e-25
18	227	16.4	192	1	BAXA_BOVIN APOPTOSIS REGULATOR BA	6.32e-25
19	226	16.3	143	1	BAXD_HUMAN BAX PROTEIN, CYTOPLASM	1.01e-24
20	226	16.3	192	1	BAXA_HUMAN APOPTOSIS REGULATOR BA	1.01e-24
21	215	15.5	218	1	BAXA_HUMAN APOPTOSIS REGULATOR BA	1.77e-22
22	214	15.4	208	1	BAK_MOUSE BCL-2 HOMOLOGOUS ANTAG	2.83e-18
23	195	14.1	177	1	NR13_COTJA APOPTOSIS REGULATOR NR	1.78e-12

24	167	12.0	172	1	BELL_MOUSE BCL2-RELATED PROTEIN A	4.51e-13
25	165	11.9	280	1	CED9_CAEEL APOPTOSIS REGULATOR CE	1.07e-12
26	162	11.7	271	1	CED9_CABBR APOPTOSIS REGULATOR CE	3.88e-12
27	159	11.5	175	1	BELL_HUMAN BCL2-RELATED PROTEIN A	1.40e-11
28	160	11.5	350	1	MCL1_HUMAN INDUCED MYELOID LEUKEM	9.12e-12
29	134	9.7	179	1	EAR_ASFE4 APOPTOSIS REGULATOR BC	4.10e-07
30	133	9.6	179	1	EAR_ASFB7 APOPTOSIS REGULATOR BC	6.09e-07
31	133	9.6	179	1	EAR_ASFB7 APOPTOSIS REGULATOR BC	6.09e-07
32	105	7.6	581	1	IRR_RAT INSULIN RECEPTOR-RELAT	2.03e-02
33	102	7.4	680	1	NOL0_RHISN MODULATION PROTEIN NOL	5.67e-02
34	99	7.1	421	1	EXG_YARLI GLUCAN 1,3-BETA-GLUCOS	1.55e-01
35	95	6.9	372	1	LIGC_TRAVE LIGNINASE C PRECURSOR	5.73e-01
36	95	6.9	647	1	NANH_MICVI SIALIDASE PRECURSOR (E	5.73e-01
37	95	6.9	843	1	PULA_THEMA PULLULANASE PRECURSOR	5.73e-01
38	94	6.8	522	1	GAG_HV2G1 GAG POLYPROTEIN [CONTA	7.89e-01
39	94	6.8	1712	1	TGFB_RAT LATENT TRANSFORMING GR	7.89e-01
40	93	6.7	603	1	GLMS_THETH GLUCOSAMINE--FRUCTOSE-	1.08e+00
41	92	6.6	262	1	NODJ_BRAJA MODULATION PROTEIN J.	1.49e+00
42	91	6.6	337	1	TALL_MOUSE TRANSALDOLASE (EC 2.2.	2.03e+00
43	91	6.6	337	1	TALL_MOUSE TRANSALDOLASE (EC 2.2.	2.03e+00
44	91	6.6	479	1	PGKC_LEIME PHOSPHOGLYCERATE KINAS	2.03e+00
45	91	6.6	520	1	YBB9_YEAST HYPOTHETICAL 59.4 KD P	2.03e+00

ALIGNMENTS

RESULT	ID	BCLW_MOUSE	STANDARD;	PRT;	193 AA.
AC	P70345;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	APOPTOSIS REGULATOR BCL-W.				
GN	BCL2L2 OR BCLW.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;				
OC	Eukarya; Rodentia; Sciurognathi; Muridae; Mus.				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 96358615.				
RA	Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,				
RA	Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;				
RT	"bcl-w, a novel member of the bcl-2 family, promotes cell survival."				
RL	Oncogene 13:665-675(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/10J;				
RX	MEDLINE; 98160183.				
RA	Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,				
RA	Russell L.D., Macgregor G.R.;				
RL	"Testicular degeneration in Bclw-deficient mice."				
RL	Nat. Genet. 18:251-256(1998).				
CC	-1- FUNCTION: PROMOTES CELL SURVIVAL.				
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.				
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND				
CC	IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,				
CC	AND SALIVARY GLAND				
CC	-1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC				
CC	FUNCTION.				
CC	-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).				
CC	-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).				
CC	-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).				
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation				
CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; U59746; AAB09056.1; -.				


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#cross-references MUID:92375724
#accession E37332
#status preliminary; nucleic acid sequence not shown; not compared with conceptual translation
#molecule_type DNA
#residues 1-33, 'E', 34-220, 'AL', 223-236 ##label EGU
GENETICS
#gene BCL2
#introns 192/3
#classification #superfamily bcl transforming protein
#keywords alternative splicing; mitochondrion; transforming protein; transmembrane protein
#length 236 #molecular-weight 26524 #checksum 6709
SUMMARY
Query Match 39.1%; Score 542; DB 1; Length 236;
Best Local Similarity 42.8%; Pred. No. 3.92e-84;
Matches 71; Conservative 45; Mismatches 44; Indels 6; Gaps 4;
Db 76 VATAGPALSPPVPCVHLTLRRAGDDFSRRYRDRFAEMSSQLHLTPFTARGRFATVVEELF 135
QY 28 VCGAGGCGPADPLHQAMRAAGDEFERFRFTSDLAQLHVTGPSAQORFTQVSDLELF 87
Db 136 RDGVNWRIVAFVFGGVMCVSNRENSPLVDNTALMTYLNRLHLHTWQDNGGWDAF 195
QY 88 QGGPNWGRIVAFVFGAALCAESVKNKEPLVGQVDWIVAYLETRLADWIHSSGGWADF 147
Db 196 VELYGP-SM---RPLDFDSWLSLKLTLSLP-WVGACITLGLAYLGHK 236
QY 148 TALYDGALEDARRREGNW-AVSTVTGVALGALVTVGAFASK 192
RESULT 11
ENTRY #type complete
TITLE transforming protein (Bcl-2) homolog - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
ACCESSIONS S24390
REFERENCE S24390
#authors Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
#journal Biochim. Biophys. Acta (1992) 1132:109-113
#title Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of the Bcl-2 oncoprotein.
#cross-references MUID:92379084
#accession S24390
#status preliminary
#molecule_type mRNA
#residues 1-232 ##label CAZ
#cross-references EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS mitochondrion; transmembrane protein
SUMMARY #length 232 #molecular-weight 25839 #checksum 1516
Query Match 39.0%; Score 540; DB 2; Length 232;
Best Local Similarity 44.3%; Pred. No. 1.01e-83;
Matches 70; Conservative 37; Mismatches 46; Indels 5; Gaps 3;
Db 79 GCAAPPGVHLALRQAGDFSRRYQRDPQMSQLHLTPFTATGRFVAVVEELFRDGNWV 138
QY 36 GPAADP-LHQAMRAAGDEFERFRFTSDLAQLHVTGPSAQORFTQVSDLEFGGPNWG 94
Db 139 RIVAFVFGGVMCVSNRENSPLVDNTATWTEYLNRLHLNHTQDNGWDAFVELYGN- 197
QY 95 RLVAFFVFGAALCAESVKNKEPLVGQVDWIVAYLETRLADWIHSSGGWADFTALYD 154
Db 198 SM---RPLDFDSWLSLKLTLSLVLVAGCITLGLAYLGHK 232
QY 155 ALEDARRREGNWAVSTVTGVALGALVTVGAFASK 192
RESULT 12
ENTRY #type complete
TITLE apoptosis regulator bcl-x - chicken
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ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
ACCESSIONS A47537
REFERENCE A47537
#authors Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson, C.B.
#journal Cell (1993) 74:597-608
#title bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.
#cross-references MUID:93364977
#accession A47537
#status preliminary
#molecule_type DNA
#residues 1-190 ##label BOI
#cross-references GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY #length 190 #molecular-weight 21467 #checksum 5509
Query Match 38.6%; Score 535; DB 2; Length 190;
Best Local Similarity 58.9%; Pred. No. 1.09e-82;
Matches 66; Conservative 21; Mismatches 24; Indels 1; Gaps 1;
Db 79 ASDVROALRDAGDEFELRYRRAFSDLTSQLHTPGTAYQSFEOVVELFHDGVNWRIVA 138
QY 39 ADPLHQAMRAAGDEFERFRFTSDLAQLHVTGPSAQORFTQVSDLEFGGPNWRLVA 98
Db 139 FFSFGGALCVESVDKEMRLVGRIVSMITTLTDHLDPIQENGWVR-TAL 189
QY 99 FFEVGAALCAESVKNKEPLVGQVDWIVAYLETRLADWIHSSGGWADFTAL 150
RESULT 13
ENTRY #type complete
TITLE apoptosis regulator bcl-x isoform - human
ALTERNATE_NAMES h-bcl-xbeta
ORGANISM #formal_name Homo sapiens #common_name man
DATE 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
ACCESSIONS JE0203
REFERENCE JE0203
#authors Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
#journal Biochem. Biophys. Res. Commun. (1998) 248:147-152
#title Identification of a human cDNA encoding a novel bcl-x isoform.
#cross-references MUID:98340865
#accession JE0203
#molecule_type mRNA
#residues 1-227 ##label BAN
#cross-references GB:U72398; NID:g1622940; PIDN:AAB17354.1; PID:g1622941
GENETICS
#gene bcl-x
#map_position 20
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY #length 227 #molecular-weight 25290 #checksum 864
Query Match 38.6%; Score 535; DB 2; Length 227;
Best Local Similarity 52.9%; Pred. No. 1.09e-82;
Matches 64; Conservative 28; Mismatches 29; Indels 0; Gaps 0;
Db 85 AVKOALREAGDEFELRYRRAFSDLTSQLHTPGTAYQSFEOVVELFHDGVNWRIVA 144
QY 41 PLHQAMRAAGDEFERFRFTSDLAQLHVTGPSAQORFTQVSDLEFGGPNWRLVA 100
Db 145 SFGGALCVESVDKEMQVLYSRIAANMATYLNHLEFWIQENGWVRTPKPLVCPFSLASQ 204
QY 101 VFGAALCAESVKNKEPLVGQVDWIVAYLETRLADWIHSSGGWADFTALYDGALEDAR 160
Db 205 R 205
```

(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:18:10 2000; Maspar time 12.63 Seconds

Tabular output not generated. 716.856 Million cell updates/sec

Title: >US-09-155-327B-9

Description: (1-192) from US09155327B.pep

Perfect Score: 1386

Sequence: 1 MPTPASTPTDTRALVADPVGY.....VTGVALGALVTVGAFVASK 192

Scoring table: PAM 150

Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir63

1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 44.905; Variance 86.927; scale 0.517

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
1	623	44.9	233	bcl-x long - mouse	5.74e-101
2	623	44.9	233	BCL-X protein - rat	5.74e-101
3	623	44.9	233	apoptosis regulator b	5.74e-101
4	585	42.2	233	BCL-X-Long - rat	4.78e-93
5	561	40.5	239	transforming protein	4.59e-88
6	556	40.1	239	transforming protein	4.98e-87
7	551	39.8	236	BCL-2 - rat (fragment	5.40e-86
8	549	39.6	236	gene bcl-2 protein -	1.40e-85
9	542	39.1	214	bcl-x transmembrane d	3.92e-84
10	542	39.1	236	transforming protein	3.92e-84
11	540	39.0	232	transforming protein	1.01e-83
12	535	38.6	190	apoptosis regulator b	1.09e-82
13	535	38.6	227	apoptosis regulator b	1.09e-82
14	503	36.3	206	transforming protein	4.22e-76
15	501	36.1	199	transforming protein	1.09e-75
16	495	35.7	216	transforming protein	1.85e-74
17	491	35.4	205	transforming protein	1.22e-73
18	404	29.1	154	gene bcl-2 protein -	5.41e-56
19	235	17.0	211	Bak protein - human	2.90e-23
20	234	16.9	211	cdn-2 protein - human	4.43e-23
21	233	16.8	192	bcl-2-associated prot	6.76e-23
22	226	16.3	143	bcl-2-associated prot	1.29e-21
23	226	16.3	192	bcl-2-associated prot	1.29e-21

ALIGNMENTS

RESULT	1
ENTRY	I49056
TITLE	bcl-x long - mouse
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
ACCESSIONS	I49056; S52866
REFERENCE	I49055
#authors	Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal	J. Immunol. (1994) 153:4388-4398
#title	Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
#cross-references	MUID:95052604
accession	I49056
status	preliminary; translated from GB/EMBL/DBJ
molecule_type	mRNA
residues	1-233 #label RES
cross-references	EMBL:U10101; NID:G506647; PIDN:AAA82173.1; PID:G506648
REFERENCE	S52866
authors	Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submission	submitted to the EMBL Data Library, November 1994
description	IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line through induction of bcl-Xl.
accession	S52866
status	preliminary
molecule_type	mRNA
residues	1-233 #label KAM
cross-references	EMBL:X83574; NID:G695622; PIDN:CAA58557.1; PID:G695623
CLASSIFICATION	#superfamily bcl transforming protein
SUMMARY	#length 233 #molecular-weight 26132 #checksum 5739
Query Match	44.9%; Score 623; DB 2; Length 233;
Best Local Similarity	52.4%; Pred. No. 5.74e-101;
Matches	76; Conservative 34; Mismatches 32; Indels 3; Gaps 3;
Db	85 AVKALREAGDEFEELRYRRAPFDSLTSLHTPTGAYGQFQVNVNELPRDGNWGRIVAFV 144
Qy	41 PLHQAMRAAGDEFEETRRRTFSDLAQAQLHVTGPAQAQRFTQVSDLELQGGFNWGRIVAFV 100
Db	145 SFGGALCVESYDKEMQVILVSRIASWMTATYLNHLEPNIQENGWDTFVDLYGNNAAESR 204
Qy	101 VFGAALCAESVKNKMEPLVGQVQDVIWVAYLETRLADWIHSSGGWADFTALYGDGALEDA 160
Db	205 KGQERFNWFTGTWVAGVLLGSL 229

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF115380; AAD13295.1; -
DR HSSP; Q07817; IMAZ.
DR PROSITE; PS01080; BHI; 1.
SQ SEQUENCE 330 AA; 35195 MW; CC87E2E0 CRC32;

Query Match 12.6%; Score 175; DB 11; Length 330;
Best Local Similarity 24.5%; Pred. No. 6.35e-14;
Matches 37; Conservative 33; Mismatches 75; Indels 6; Gaps 6;

Db 160 ELISRY-LREQATSKDAKPLGEAGAGRALETERRVGDGVQVORNHETAFQGLRKLKLDIK 218

QY 16 DFVG-YRLKQKGYVC-GAGP-GE-GPAADPLHQAMRAAGDEFEFRFTFSDLAALHVT 71

Db 219 NEDDVKSFRVMTVHFQKGVNMGRIVLISFGAFVAKHLKSINOESCIEPLAESITDVL 278

QY 72 PGSAQQRFTQVSDLELFGQG-PNWGRVLAFFVFGAALCAESVKNEMEPLVGVQVQDWIVAYL 130

Db 279 VTKRDWLVKQKRGDGFVEFFHVQDEGGIR 309

QY 131 ETRLADWTHSSGGWADFTALYGDGALEDARR 161

Query Match 12.1%; Score 168; DB 13; Length 211;
Best Local Similarity 22.7%; Pred. No. 1.23e-12;
Matches 30; Conservative 31; Mismatches 70; Indels 1; Gaps 1;

Db 55 PGRASSAVMEKALETLRRYVGDGVQVQKHELAFGQMLRKLKLEIKKEDDLQAVCEVAQAQVNDG 114

QY 31 AGPGCPAADPLHQAMRAAGDEFEFRFTFSDLAALHVTGSAQQRFTQVSDLELFGQG 90

Db 115 VTWNGRVTLISGAFVAKHLKSINOECITSLAGIITDALVSSKREWLMSOGGEGFVD 174

QY 91 -PNWGRVLAFFVFGAALCAESVKNEMEPLVGVQVQDWIVAYLETRLADWTHSSGGWADFTALY 149

Db 175 FFRVEDLESSIR 186

QY 150 LYGDGALEDARR 161

Query Match 12.1%; Score 168; DB 13; Length 211;
Best Local Similarity 22.7%; Pred. No. 1.23e-12;
Matches 30; Conservative 31; Mismatches 70; Indels 1; Gaps 1;

Db 55 PGRASSAVMEKALETLRRYVGDGVQVQKHELAFGQMLRKLKLEIKKEDDLQAVCEVAQAQVNDG 114

QY 31 AGPGCPAADPLHQAMRAAGDEFEFRFTFSDLAALHVTGSAQQRFTQVSDLELFGQG 90

Db 115 VTWNGRVTLISGAFVAKHLKSINOECITSLAGIITDALVSSKREWLMSOGGEGFVD 174

QY 91 -PNWGRVLAFFVFGAALCAESVKNEMEPLVGVQVQDWIVAYLETRLADWTHSSGGWADFTALY 149

Db 175 FFRVEDLESSIR 186

QY 150 LYGDGALEDARR 161

Query Match 12.1%; Score 168; DB 13; Length 211;
Best Local Similarity 22.7%; Pred. No. 1.23e-12;
Matches 30; Conservative 31; Mismatches 70; Indels 1; Gaps 1;

Db 55 PGRASSAVMEKALETLRRYVGDGVQVQKHELAFGQMLRKLKLEIKKEDDLQAVCEVAQAQVNDG 114

QY 31 AGPGCPAADPLHQAMRAAGDEFEFRFTFSDLAALHVTGSAQQRFTQVSDLELFGQG 90

Db 115 VTWNGRVTLISGAFVAKHLKSINOECITSLAGIITDALVSSKREWLMSOGGEGFVD 174

QY 91 -PNWGRVLAFFVFGAALCAESVKNEMEPLVGVQVQDWIVAYLETRLADWTHSSGGWADFTALY 149

Db 175 FFRVEDLESSIR 186

QY 150 LYGDGALEDARR 161

Query Match 12.1%; Score 168; DB 13; Length 211;
Best Local Similarity 22.7%; Pred. No. 1.23e-12;
Matches 30; Conservative 31; Mismatches 70; Indels 1; Gaps 1;

Db 55 PGRASSAVMEKALETLRRYVGDGVQVQKHELAFGQMLRKLKLEIKKEDDLQAVCEVAQAQVNDG 114

QY 31 AGPGCPAADPLHQAMRAAGDEFEFRFTFSDLAALHVTGSAQQRFTQVSDLELFGQG 90

Db 115 VTWNGRVTLISGAFVAKHLKSINOECITSLAGIITDALVSSKREWLMSOGGEGFVD 174

QY 91 -PNWGRVLAFFVFGAALCAESVKNEMEPLVGVQVQDWIVAYLETRLADWTHSSGGWADFTALY 149

Db 175 FFRVEDLESSIR 186

QY 150 LYGDGALEDARR 161

Query Match 12.1%; Score 168; DB 13; Length 211;
Best Local Similarity 22.7%; Pred. No. 1.23e-12;
Matches 30; Conservative 31; Mismatches 70; Indels 1; Gaps 1;

Db 55 PGRASSAVMEKALETLRRYVGDGVQVQKHELAFGQMLRKLKLEIKKEDDLQAVCEVAQAQVNDG 114

QY 31 AGPGCPAADPLHQAMRAAGDEFEFRFTFSDLAALHVTGSAQQRFTQVSDLELFGQG 90

Db 115 VTWNGRVTLISGAFVAKHLKSINOECITSLAGIITDALVSSKREWLMSOGGEGFVD 174

QY 91 -PNWGRVLAFFVFGAALCAESVKNEMEPLVGVQVQDWIVAYLETRLADWTHSSGGWADFTALY 149

Db 175 FFRVEDLESSIR 186

QY 150 LYGDGALEDARR 161

Query Match 12.1%; Score 168; DB 13; Length 211;
Best Local Similarity 22.7%; Pred. No. 1.23e-12;
Matches 30; Conservative 31; Mismatches 70; Indels 1; Gaps 1;

Db 55 PGRASSAVMEKALETLRRYVGDGVQVQKHELAFGQMLRKLKLEIKKEDDLQAVCEVAQAQVNDG 114

QY 31 AGPGCPAADPLHQAMRAAGDEFEFRFTFSDLAALHVTGSAQQRFTQVSDLELFGQG 90

Db 115 VTWNGRVTLISGAFVAKHLKSINOECITSLAGIITDALVSSKREWLMSOGGEGFVD 174

QY 91 -PNWGRVLAFFVFGAALCAESVKNEMEPLVGVQVQDWIVAYLETRLADWTHSSGGWADFTALY 149

Db 175 FFRVEDLESSIR 186

QY 150 LYGDGALEDARR 161

Query Match 12.1%; Score 168; DB 13; Length 211;
Best Local Similarity 22.7%; Pred. No. 1.23e-12;
Matches 30; Conservative 31; Mismatches 70; Indels 1; Gaps 1;

Db 55 PGRASSAVMEKALETLRRYVGDGVQVQKHELAFGQMLRKLKLEIKKEDDLQAVCEVAQAQVNDG 114

QY 31 AGPGCPAADPLHQAMRAAGDEFEFRFTFSDLAALHVTGSAQQRFTQVSDLELFGQG 90

Db 115 VTWNGRVTLISGAFVAKHLKSINOECITSLAGIITDALVSSKREWLMSOGGEGFVD 174

QY 91 -PNWGRVLAFFVFGAALCAESVKNEMEPLVGVQVQDWIVAYLETRLADWTHSSGGWADFTALY 149

Db 175 FFRVEDLESSIR 186

QY 150 LYGDGALEDARR 161

GN BAK.

OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]

RP SEQUENCE FROM N.A.

RA BARTLING B., HOFFMANN J., HOLTZ J., SCHULZ R., HEUSCH G., DARMER D.;

RT "Expression of apoptosis-associated genes in hibernating and stunned

RL myocardium of pig.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ001204; CAA04598.1; -

DR HSSP; Q16611; 1BXL.

DR PROSITE; PS01259; BH3; 1.

DR PFAM; PF00452; Bcl-2; 1.

KT Apoptosis.

FT NON_TER 1 1

FT NON_TER 80 80

SQ SEQUENCE 80 AA; 8818 MW; 973BE2D0 CRC32;

Query Match 10.4%; Score 144; DB 6; Length 80;
Best Local Similarity 35.4%; Pred. No. 2.28e-08;
Matches 17; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Db 33 GDDINRRYDSEFQAMLOHLOPTAENAYEYFTKIASSLFESGINWGVV 80

QY 50 GDEPETFRRFTSDLAALHVTGSAQQRFTQVSDLELFGGPNWGRV 97

Result 15

ID O55178 PRELIMINARY; PRT; 128 AA.

DT O55178; AC O55178;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

DE B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN ALC (ALC PROTEIN).

GN BCL2A1C OR ALC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-129/SV; TISSUE=LIVER;

RA HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,

RA NAKAYAMA K., NAKAYAMA K.-I.;

RL Int. Immunol. 0:0-0(1998).

DR EMBL; U23779; AAB97955.1; -

DR MGD; MGI:1278327; Bcl2alc.

DR PROSITE; PS01080; BHI; 1.

DR PFAM; PF00452; Bcl-2; 1.

SQ SEQUENCE 128 AA; 14763 MW; DF4F2653 CRC32;

Query Match 8.7%; Score 120; DB 11; Length 128;
Best Local Similarity 38.1%; Pred. No. 2.21e-04;
Matches 16; Conservative 12; Mismatches 12; Indels 2; Gaps 2;

Db 58 DFHVESIDTTRIFNQVMEKEFEFGIINWGRIVTIFAPGVV 99

QY 67 QLHVTP-GSAQQRFTQVSDLELFGGP-NWGRVLAFFVFGAAL 106

Search completed: Fri Jun 23 14:19:38 2000
Job time : 25 secs.

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF051928.1; - 79B4BBE6 CRC32;
 SQ SEQUENCE 170 AA; 18729 MW; 79B4BBE6 CRC32;

Query Match 12.7%; Score 176; DB 11; Length 170;
 Best Local Similarity 25.0%; Pred. No. 4.14e-14;
 Matches 28; Conservative 35; Mismatches 47; Indels 2; Gaps 2;
 Db 21 SPTDELVAQAALGVEYVHARLLRAGLSWASAPASGGL-RLAEVCTVLLRLGIWNG 79
 QY 36 GPAADPLHQAARAAAGDEF-ETFRFTFSDLAQLHVFSGAQRFTQVSDLEFGGPNWG 94
 Db 80 KVSLSYVAAGLAVDCVROAQPAMVHALVDCIGFVVKTLATWLRRRGWTD 131
 QY 95 RLVAFFVFGAALCAESVNKEMEPLVGQVDWIVAYLETRLADWIHSSGGWAD 146

RESULT 9
 ID O55177 PRELIMINARY; PRT; 172 AA.

AC O55177;
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN AIB (A1-B PROTEIN).
 GN BCL2A1B OR A1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SV; TISSUE=LIVER;
 RA HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
 RA NAKAYAMA K., NAKAYAMA K.-I.;
 RL Int. Immunol. 0:0-0(1998).
 DR EMBL: U23778; AAB97954.1; -
 DR EMBL: U23777; AAB97954.1; JOINED.
 DR MGD: MGI-1278326; Bcl2a1b.
 DR PROSITE; PS01080; BHI; 1.
 DR PFAM; PF00452; Bcl-2; 1.
 SQ SEQUENCE 172 AA; 20048 MW; FA16DF6C CRC32;

Query Match 12.6%; Score 175; DB 11; Length 172;
 Best Local Similarity 33.7%; Pred. No. 6.35e-14;
 Matches 29; Conservative 20; Mismatches 30; Indels 7; Gaps 5;

Db 58 DFHVESIDTARIIFNOVMEKEFEFGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
 QY 67 QLVHTP-GSAQRFTQVSDLEFGGP-NWGRVLAFFVFGAALCAESVNKEMEPL-VG--- 120
 Db 117 QVSFVAEFFIINWGWIRNGWED 142
 QY 121 QVDWIVAYLETRLADWIHSSGGWAD 146

RESULT 10
 ID O55179 PRELIMINARY; PRT; 172 AA.

AC O55179;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN AIB (A1-D PROTEIN).
 GN BCL2A1D OR A1D.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SV; TISSUE=LIVER;
 RA HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
 RA NAKAYAMA K., NAKAYAMA K.-I.;
 RL Int. Immunol. 0:0-0(1998).
 DR EMBL: U23781; AAB97956.1; -
 DR EMBL: U23780; AAB97956.1; JOINED.

DR MGD: MGI-1278325; Bcl2a1d.
 DR PROSITE; PS01080; BHI; 1.
 DR PFAM; PF00452; Bcl-2; 1.
 SQ SEQUENCE 172 AA; 20048 MW; 1B340DDD CRC32;

Query Match 12.6%; Score 174; DB 11; Length 172;
 Best Local Similarity 33.7%; Pred. No. 9.71e-14;
 Matches 29; Conservative 20; Mismatches 30; Indels 7; Gaps 5;
 Db 58 DFHVESIDTARIIFNOVMEKEFEFGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
 QY 67 QLVHTP-GSAQRFTQVSDLEFGGP-NWGRVLAFFVFGAALCAESVNKEMEPL-VG--- 120
 Db 117 QVSFVAEFFIINWGWIRNGWED 142
 QY 121 QVDWIVAYLETRLADWIHSSGGWAD 146

RESULT 11
 ID O9W6F2 PRELIMINARY; PRT; 174 AA.

AC O9W6F2;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE PROTEIN A1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 99190706.
 RA LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.;
 RT "Role of Nr13 in regulation of programmed cell death in the bursa of
 RT Fabricius";
 RL Genes Dev. 13:718-728(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA SOFER L., BURNSIDE J.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF120211; RAD31645.1; -
 SQ SEQUENCE 174 AA; 20095 MW; 70F5FDAA CRC32;

Query Match 12.6%; Score 174; DB 13; Length 174;
 Best Local Similarity 24.4%; Pred. No. 9.71e-14;
 Matches 30; Conservative 33; Mismatches 52; Indels 8; Gaps 6;

Db 27 GPAQTFVAVHLNLIASSLQDQTEEARLPDLRIDITSDVAKRIFNGVMEKFAAGNTNW 86
 QY 36 GPAADPLHQAARAAAGDEFETFRFTFSDLAQLHVTGSAQQR-FTQVSDLEFGGPNW 93
 Db 87 GRIMTIFTFGLL-TKKLQEHGVLTGEKEKISYFITEYIINNKAAWIDANGWENGFL 145
 QY 94 GRUVAFFVFGAALCAESVNKEMEPLVGQVDWI---VA-YLETRLADWIHSSGGWAD-FT 148
 Db 146 TKF 148
 QY 149 ALY 151

RESULT 12
 ID Q9Z1P3 PRELIMINARY; PRT; 330 AA.

AC Q9Z1P3;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MCL-1 PROTEIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA LEO C.P., HSU S.Y., HSUEH A.J.W.;
 RT "Sequence of rat Mcl-1, a Bcl-2-related gene.";

RESULT	8
ID	088857 PRELIMINARY; PRT; 170 AA.
AC	088857;
DT	01-NOV-1998 (TREMBLrel. 08, Created)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE	BCL-2 RELATED OVARIAN KILLER PROTEIN.
GN	BOK.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=OVARY, UTERUS;
RX	MEDLINE; 9802143.
RA	HU S.Y., KAIPTA A., MCCEE E., LOWELI M., HSUEH A.J.;
RT	"Bok is a pro-apoptotic Bcl-2 protein with restricted expression in
RT	reproductive tissues and heterodimerizes with selective anti-apoptotic
RT	Bcl-2 family members.";
RL	Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=OVARY, UTERUS;
RA	HU S.Y., HSUEH A.J.W.;
RT	"A splicing variant of the Bcl-2 member Bok with a truncated BH3
RT	domain induces apoptosis without dimerization with anti-apoptotic Bcl-
RT	2 proteins.";

```
QY 180 GALVTGGAFFASK 192
RESULT 2
ID O35844 PRELIMINARY; PRT; 233 AA.
AC O35844;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE BCL2-LIKE (BCL-XL).
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=THYMUS;
RX MEDLINE; 98051053.
RA YANG X.-F., WEBER G.F., CANTOR H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
RT apoptosis in T cells.";
DR EMBL; 051278; AAC53459.1; -.
DR HSSP; P53563; IAF3.
DR MGD; MGI:88139; Bcl2l.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PFAM; PF00452; Bcl-2; 1.
SQ SEQUENCE 233 AA; 26033 MW; A4A14278 CRC32;

Query Match 46.0%; Score 638; DB 11; Length 233;
Best Local Similarity 53.1%; Pred. No. 2.64e-113; Indels 3; Gaps 3;
Matches 77; Conservative 34; Mismatches 31;

Db 85 AVKQALREAGDEFELRYRAFSDLTSQLHTTGTAYQSFQVNVNLEFRDGVNWRIVAF 144
QY 41 PLHQAMRAAGDEFETFRRTFSDLAQLHVTGPSAQORFTQVSDLEFGQGNWRLVAF 100
Db 145 SFGGALCVESVDKEMQVLSRTASMAIYLNHLEPWQIENGWDTFVDLYGNNAAESR 204
QY 101 VFGAALCAESVNKEMEPVGVQVDWIVAYLETRLADWIHSSGGWADFALYGDGALE 160
Db 205 KGKEGFNRWELTGMTVAGVWLLGSL 229
QY 161 RLREG-N-WAVSTV-VTGAVALGAL 182

RESULT 3
ID O02718 PRELIMINARY; PRT; 229 AA.
AC O02718;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE BCL-2 (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOLSTEIN; TISSUE=THYMUS;
RA REYES R.A., COCKERELL G.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92434; AAB53319.1; -.
DR HSSP; P53563; IAF3.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PFAM; PF00452; Bcl-2; 1.
FT NON_TER 229

SQ SEQUENCE 229 AA; 25099 MW; E82B3DFB CRC32;

Query Match 40.4%; Score 560; DB 6; Length 229;
Best Local Similarity 42.7%; Pred. No. 1.15e-95;
Matches 70; Conservative 48; Mismatches 40; Indels 6; Gaps 4;

Db 71 AAGPAPSPVPVPHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTTAREFATVVEELFRD 130
QY 30 GAGPGEPAADPLHQAMRAAGDEFETFRRTFSDLAQLHVTGPSAQORFTQVSDLEFG 89
Db 131 GVNWRIVAFEFEGGVCVSVNREMSPLVDSIALNMTYELNHLHTWQDNGWDVAF 190
QY 90 GPNWGLVAFVFGAALCAESVNKEMEPVGVQVDWIVAYLETRLADWIHSSGGWADF 149
Db 191 LYGP-SM--RPLDFSWLSLKALLSLAL-VGACITLGLAYLGHK 229
QY 150 LYGDGALEDARRLRGNW-AVSTVTVTGAVALGALVTGGAFFASK 192

RESULT 4
ID O35843 PRELIMINARY; PRT; 235 AA.
AC O35843;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE BCL2-LIKE (BCL-X-GAMMA).
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=THYMUS;
RX MEDLINE; 98051053.
RA YANG X.-F., WEBER G.F., CANTOR H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
RT apoptosis in T cells.";
DR EMBL; U51277; AAC53458.1; -.
DR HSSP; P53563; IAF3.
DR MGD; MGI:88139; Bcl2l.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PFAM; PF00452; Bcl-2; 1.
SQ SEQUENCE 235 AA; 26122 MW; FB0B0207 CRC32;

Query Match 38.5%; Score 533; DB 11; Length 235;
Best Local Similarity 58.1%; Pred. No. 1.32e-89;
Matches 61; Conservative 25; Mismatches 19; Indels 0; Gaps 0;

Db 85 AVKQALREAGDEFELRYRAFSDLTSQLHTTGTAYQSFQVNVNLEFRDGVNWRIVAF 144
QY 41 PLHQAMRAAGDEFETFRRTFSDLAQLHVTGPSAQORFTQVSDLEFGQGNWRLVAF 100
Db 145 SFGGALCVESVDKEMQVLSRTASMAIYLNHLEPWQIENGW 189
QY 101 VFGAALCAESVNKEMEPVGVQVDWIVAYLETRLADWIHSSGGW 145

RESULT 5
ID Q9WU15 PRELIMINARY; PRT; 170 AA.
AC Q9WU15;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE BCL-X SHORT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
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WQ5REL4 (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:19:13 2000; MasPar time 19.74 Seconds

Tabular output not generated. 674,404 Million cell updates/sec

Title: >US-09-155-327B-9
Description: (1-192) from US09155327B.pep
Perfect Score: 1386

Sequence: 1 MPTPASTPDRALVADFGV.....VTGVALGALVTGGAFFASK 192

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 44.372; Variance 79.166; scale 0.560

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	1343	96.9	193	11	O88996 BCL-W.	3.25e-277
2	638	46.0	233	11	O35844 BCL2-LIKE (BCL-XL).	2.64e-113
3	560	40.4	229	6	O02718 BCL-2 (FRAGMENT).	1.15e-95
4	533	38.5	235	11	O35843 BCL2-LIKE (BCL-X-GAMMA	1.32e-89
5	207	14.9	170	11	O9WU15 BCL-X SHORT.	5.41e-20
6	182	13.1	213	11	O35425 BCL-2-RELATED OVARIAN	3.16e-15
7	177	12.8	331	11	P97287 EAT/MCL-1 PROTEIN (MCL	2.70e-14
8	176	12.7	170	11	O88857 BCL-2-RELATED OVARIAN	4.14e-14
9	175	12.6	172	11	O55177 B-CELL LEUKEMIA/LYMPHO	6.35e-14
10	174	12.6	172	11	O55179 B-CELL LEUKEMIA/LYMPHO	9.71e-14
11	174	12.6	174	13	O9W6F2 PROTEIN AL.	9.71e-14
12	175	12.6	330	11	O921P3 MCL-1 PROTEIN.	6.35e-14
13	168	12.1	211	13	O9W6F1 MYELOID CELL LEUKEMIA	1.23e-12
14	144	10.4	80	6	O77738 BAK PROTEIN (FRAGMENT)	2.28e-08
15	120	8.7	128	11	O55178 B-CELL LEUKEMIA/LYMPHO	2.21e-04
16	117	8.4	923	4	O9V3R2 NUCLEAR TRANSPORT RECE	6.59e-04
17	103	7.4	168	14	O36423 SIMILAR TO BCL-FAMILY	8.67e-02
18	103	7.4	521	14	O9VTU1 GAG PROTEIN.	1.21e-01
19	102	7.4	1259	5	O44971 C42C1.4 PROTEIN.	2.34e-01
20	100	7.2	630	5	O24222 METALLOPEPTIDASE.	

21	99	7.1	175	14	P90504	ORF 16.	3.25e-01
22	98	7.1	187	14	O9WRT6	BCL-2 HOMOLOG.	4.50e-01
23	98	7.1	975	4	O3Y5L0	TRANSPORTIN-SR.	4.50e-01
24	97	7.0	256	2	O9Z657	MORPHINE 6-DEHYDROGENA	6.22e-01
25	97	7.0	597	14	O9YUR4	TERMINAL PROTEIN.	6.22e-01
26	97	7.0	798	1	O59515	798AA LONG HYPOTHETICA	6.22e-01
27	97	7.0	967	5	O18965	D2013.5 PROTEIN.	6.22e-01
28	97	7.0	1937	2	O30482	PKS MODULE 4.	6.22e-01
29	96	6.9	1713	11	O88349	LATENT TGF BETA BINDIN	8.57e-01
30	94	6.8	279	14	O57148	SEROTYPE B PUTATIVE MA	1.62e+00
31	94	6.8	289	2	O51585	HYPOTHETICAL 32.3 KD P	1.62e+00
32	94	6.8	494	2	P95148	HYPOTHETICAL 53.6 KD P	1.62e+00
33	94	6.8	728	10	O04512	SEQUENCE OF BAC F2M12	1.62e+00
34	94	6.8	757	14	O37361	PUTATIVE RNA DEPENDENT	1.62e+00
35	94	6.8	3104	2	O04846	FATTY ACID SYNTHASE (E	1.62e+00
36	93	6.7	262	2	O92312	NODJ.	2.21e+00
37	93	6.7	440	1	O9YFI3	440AA LONG HYPOTHETICA	2.21e+00
38	93	6.7	555	4	O9Y625	GLYPICAN-6.	2.21e+00
39	93	6.7	657	2	O07192	HYPOTHETICAL 70.8 KD P	2.21e+00
40	91	6.6	140	11	P07003	TRANSALDOLASE 1 (EC 2.	4.10e+00
41	91	6.6	337	4	O00751	TRANSALDOLASE (EC 2.2.	4.10e+00
42	92	6.6	413	2	P94131	CIS,CIS-MONONATE TRANS	3.01e+00
43	91	6.6	505	1	O27209	CONSERVED PROTEIN (FLP	4.10e+00
44	91	6.6	896	1	O30061	MOLYBDOPTEIN OXIDORED	4.10e+00
45	91	6.6	4101	5	O02425	R31.1 PROTEIN.	4.10e+00

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	193 AA.
ID	O88996			
AC	O88996;			
DT	01-NOV-1998 (Tremblrel. 08, Created)			
DT	01-NOV-1998 (Tremblrel. 08, Last sequence update)			
DT	01-NOV-1999 (Tremblrel. 12, Last annotation update)			
DE	BCL-W.			
GN	BCL-W.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
[1]				
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;			
RA	HAMNER S., SKOGLOSA Y., LINDHOLM D.;			
RT	"Differential expression of Bcl-w and Bcl-x mRNA in the developing and adult nervous system.";			
RL	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF096291; AAC64200.1; -			
DR	HSSP; P53563; 1AF3.			
DR	PROSITE; PS01080; BH1; 1.			
DR	PROSITE; PS01258; BH2; 1.			
DR	PROSITE; PS01260; BH4_1; 1.			
DR	PFAM; PF00452; Bcl-2; 1.			
SQ	SEQUENCE 193 AA; 20820 MW; 6E5F84BA CRC32;			

Query Match	96.98;	Score 1343;	DB 11;	Length 193;
Best Local Similarity	95.38;	Pred. No. 3.25e-277;		
Matches 184;	Conservative 7;	Mismatches 1;	Indels 1;	Gaps 1;
Db	1	MATPASTPDRALVADFGVYKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT	60	
Qy	1	MPTPASTPDRALVADFGVYKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT	60	
Db	61	FSDLAALQHLVTPGSAQORFTQVSDQLPQGGPNNGRLVAFVFFGAALCAESVNMKEPLVG	120	
Qy	61	FSDLAALQHLVTPGSAQORFTQVSDQLPQGGPNNGRLVAFVFFGAALCAESVNMKEPLVG	120	
Db	121	QVQDWMTYLETRLADWHSSGGWAETALYGGALAEARRLRGNWASVRYTLTGAVL	180	
Qy	121	QVQDWMTYLETRLADWHSSGGWAETALYGGALAEARRLRGNWASVRYTLTGAVL	179	
Db	181	GALVTVGGAFFASK	193	

CC APPLICANT: BARR, PHILIP J.
CC TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
CC TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: MORRISON & FOERSTER
CC STREET: 755 Page Mill Road
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94304-1018
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/471,057
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/320,157
CC FILING DATE: 07-OCT-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: LEHNHARDT, SUSAN K.
CC REGISTRATION NUMBER: 33,943
CC REFERENCE/DOCKET NUMBER: 23647-20007.20
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 813-5600
CC TELEFAX: (415) 494-0792
CC TELEX: 706141
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 233 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC SEQUENCE 233 AA; 26049 MW; 275801 CN;
SQ
Query Match 44.9%; Score 623; DB 3; Length 233;
Best Local Similarity 52.4%; Pred. No. 7.82e-45;
Matches 76; Conservative 34; Mismatches 32; Indels 3; Gaps 3;
Db 85 AVKQALREAGDEFELRYRAFSDLTSQLHTPGTAYQSFQVNVNLFPRDGVNWRIVAFF 144
QY 41 PLHQAMRAAGDEFETFRRTFSDLAQLHVTGSAQQRFTQVSDLFQGGPNWGRIVAFF 100
Db 145 SFGGALCVESVDKEMQVLVSRIAAMATYLNHLEPWIQENGWDTFVELYGNNAAESR 204
QY 101 VFGAALCAESVKNEMPLVGQVQDVIYVLETRLDADWIHSSGGWADFTALYDGALEDAR 160
Db 205 KGQERFNWFLTGMTVAGVVLGSL 229
QY 161 RLREG-N-WAVSTV-VTGAVALGAL 182
RESULT 13
ID US-08-333-565-59 STANDARD; PRT; 233 AA.
XX
AC xxxxxx
XX
DT
DE
Sequence 59, Application US/08333565
XX
Sequence 59, Application US/08333565
CC Patent No. 5622852
CC GENERAL INFORMATION:
CC APPLICANT: KORSMEYER, Stanley J.
CC TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
CC TITLE OF INVENTION: REGULATOR
CC NUMBER OF SEQUENCES: 59
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/333,565
CC FILING DATE: 31-OCT-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15726A-000700
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 59:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 233 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: peptide
CC SEQUENCE 233 AA; 26049 MW; 275801 CN;
SQ
Query Match 44.9%; Score 623; DB 1; Length 233;
Best Local Similarity 52.4%; Pred. No. 7.82e-45;
Matches 76; Conservative 34; Mismatches 32; Indels 3; Gaps 3;
Db 85 AVKQALREAGDEFELRYRAFSDLTSQLHTPGTAYQSFQVNVNLFPRDGVNWRIVAFF 144
QY 41 PLHQAMRAAGDEFETFRRTFSDLAQLHVTGSAQQRFTQVSDLFQGGPNWGRIVAFF 100
Db 145 SFGGALCVESVDKEMQVLVSRIAAMATYLNHLEPWIQENGWDTFVELYGNNAAESR 204
QY 101 VFGAALCAESVKNEMPLVGQVQDVIYVLETRLDADWIHSSGGWADFTALYDGALEDAR 160
Db 205 KGQERFNWFLTGMTVAGVVLGSL 229
QY 161 RLREG-N-WAVSTV-VTGAVALGAL 182
RESULT 14
ID US-08-081-448-6 STANDARD; PRT; 233 AA.
XX
AC xxxxxx
XX
DT
DE
Sequence 6, Application US/08081448
XX
Sequence 6, Application US/08081448
CC Patent No. 5646008
CC GENERAL INFORMATION:
CC APPLICANT: Thompson, Craig B.
CC APPLICANT: Boise, Lawrence H.
CC TITLE OF INVENTION: Vertebrate Apoptosis Gene:
CC TITLE OF INVENTION: Compositions and Methods
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: 321 No. 5646008th Clark Street, Suite 800
CC CITY: Chicago
CC STATE: IL
CC COUNTRY: USA
CC ZIP: 60610
CC COMPUTER READABLE FORM:
CC

Db 61 SDLAALHVTGSAQQRFTQVSDLEFGGPNWGLVAFVFGAALCAESVKNKEPVLVG 120
Qy 62 SDLAALHVTGSAQQRFTQVSDLEFGGPNWGLVAFVFGAALCAESVKNKEPVLVG 121
Db 121 VOEWVAYLETRLDWIHSSGGMAEFTALYGDGALEARRLRGNWASVRTLVTGVALG 180
Qy 122 VQDWIVAYLETRLDWIHSSGGWADFTALYGDGALEARRLRGNWA-VSTVVTGVALG 180
Db 181 ALVTGGAFFASK 192
Qy 181 ALVTGGAFFASK 192
RESULT 8
ID US-08-798-897-6 STANDARD; PRT; 192 AA.
XX
AC xxxxxx
XX
XX
DT
XX
DE
XX
CC Sequence 6, Application US/08798897
CC Patent No. 5789201
CC GENERAL INFORMATION:
CC APPLICANT: Guastella, John
CC TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
CC TITLE OF INVENTION: Homologue
CC NUMBER OF SEQUENCES: 53
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC STREET: 1100 New York Avenue, N.W., Suite 600
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/798,897
CC FILING DATE: February 11, 1997
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Esmond, Robert W.
CC REGISTRATION NUMBER: 32,893
CC REFERENCE/DOCKET NUMBER: 1483.0140001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-371-2600
CC TELEFAX: 202-371-2540
CC INFORMATION FOR SEQ ID NO: 6:
CC LENGTH: 192 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 192 AA; 20701 MW; 181510 CN;
Query Match 95.7%; Score 1326; DB 1; Length 192;
Best Local Similarity 94.3%; Pred. No. 2.79e-109;
Matches 181; Conservative 8; Mismatches 2; Indels 1; Gaps 1;
Db 1 ATPASAPTRALVDFVGYKLRQYVCGAGGEGPADPLHQAMRAAGDEFETRFRRTF 60
Qy 2 PTPASTPTRALVDFVGYRLRQYVCGAGGEGPADPLHQAMRAAGDEFETRFRRTF 61
Db 61 SDLAALHVTGSAQQRFTQVSDLEFGGPNWGLVAFVFGAALCAESVKNKEPVLVG 120
Qy 62 SDLAALHVTGSAQQRFTQVSDLEFGGPNWGLVAFVFGAALCAESVKNKEPVLVG 121

Db 121 VOEWVAYLETRLDWIHSSGGMAEFTALYGDGALEARRLRGNWASVRTLVTGVALG 180
Qy 122 VQDWIVAYLETRLDWIHSSGGWADFTALYGDGALEARRLRGNWA-VSTVVTGVALG 180
Db 181 ALVTGGAFFASK 192
Qy 181 ALVTGGAFFASK 192
RESULT 9
ID PCT-US95-04600-24 STANDARD; PRT; 233 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
CC Sequence 24, Application PC/TUS9504600
CC Sequence 24, Application PC/TUS9504600
CC GENERAL INFORMATION:
CC APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
CC TITLE OF INVENTION: Interaction of Proteins Involved in
CC TITLE OF INVENTION: a Cell Death Pathway
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Campbell and Flores
CC STREET: 4370 La Jolla Village Drive, Suite 700
CC CITY: San Diego
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92122
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/04600
CC FILING DATE: 12-APR-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Imbra, Richard J.
CC REGISTRATION NUMBER: 37,643
CC REFERENCE/DOCKET NUMBER: EP-LJ 1361
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 535-9001
CC TELEFAX: (619) 535-8949
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 233 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 233 AA; 26063 MW; 275311 CN;
Query Match 44.9%; Score 623; DB 4; Length 233;
Best Local Similarity 52.4%; Pred. No. 7.82e-45;
Matches 76; Conservative 34; Mismatches 32; Indels 3; Gaps 3;
Db 85 AVKQALREAGDEFELRYRAFSDLTSQLHITPGATQVSEQVYVNFRLRGVNWGRIVAF 144
Qy 41 PLHQAMRAAGDEFETRFRRTFSDLAALHVTGSAQQRFTQVSDLEFGGPNWGLVAF 100
Db 145 SFGALCVSEYDKEMQVLSRIAANWATYLNHLEPWIOENGWDTFVELYGNNAAESR 204
Qy 101 VFGAALCAESVKNKEPVLVGQVQDWIVAYLETRLDWIHSSGGWADFTALYGDGALEARR 160
Db 205 KGQERENRNFELTGMTVAGVLLGSL 229
Qy 161 RLREG-N-WAVSTV-VTGAVALGAL 182
RESULT 10

Db	1	ATPASTPDTRALVADFGVYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRFRRTF	60
Qy	2	PTPASTPDTRALVADFGVYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFTFRFRRTF	61
Db	61	SDLAAQLHVTTPGSNAQRFTQVSDLEFQGGPNWGRGLVAFVFGGAALCAESYNKEMEPLVGQ	120
Qy	62	SDLAAQLHVTTPGSNAQRFTQVSDLEFQGGPNWGRGLVAFVFGGAALCAESYNKEMEPLVGQ	121
Db	121	VQDWMMVYLETRLADWTHSSGGWAEFTALYGDGCALEARLRREGNWSVRTVLTGAVALLG	180
Qy	122	VQDWIVAYLETRLADWTHSSGGWADFTALYGDGALEDARRLRREGNWA-VSTVVVGAVALLG	180
Db	181	ALVTGGAFFASK 192	
Qy	181	ALVTGGAFFASK 192	
RESULT	6		
ID	US-08-798-897-5	STANDARD;	PRT; 192 AA.
XX	xxxxxx		
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DT			
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DE			
CC	Sequence 5, Application US/08798897		
CC	Sequence 5, Application US/08798897		
CC	Patent No. 5789201		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Guastella, John		
CC	TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2		
CC	TITLE OF INVENTION: Homologue		
CC	NUMBER OF SEQUENCES: 53		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.		
CC	STREET: 1100 New York Avenue, N.W., Suite 600		
CC	CITY: Washington		
CC	STATE: DC		
CC	COUNTRY: USA		
CC	ZIP: 20005		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/798,897		
CC	FILING DATE: February 11, 1997		
CC	CLASSIFICATION: 435		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Esmond, Robert W.		
CC	REGISTRATION NUMBER: 32,893		
CC	REFERENCE/DOCKET NUMBER: 1483.0140001		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: 202-371-2600		
CC	TELEFAX: 202-371-2540		
CC	INFORMATION FOR SEQ ID NO: 5:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 192 amino acids		
CC	TYPE: amino acid		
CC	STRANDEDNESS: not relevant		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: protein		
CC	SEQUENCE 192 AA; 20689 MW; 183185 CN;		
SQL			

Db	61	SDLAQLHVTGPGSAQRTQTVDSELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ	120
Qy	62	SDLAQLHVTGPGSAQRTQTVDSELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ	121
Db	121	VODMWYIETRDLADWIHSSGGWAFFETALYCDGALEARLRRCGNWASVRTVLGTGAVALG	180
Qy	122	VODMIVAYLETRDLADWIHSSGGWADFETALYGDGALEDARLRREGNWA-VSTVVVTGVAVALG	180
Db	181	ALVTGVGAFFASK	192
Qy	181	ALVTGVGAFFASK	192
RESULT	7		
ID	US-08-978-523-6	STANDARD:	PRT; 192 AA.
XX	xxxxxx		
AC			
XX			
DT			
XX			
DE	Sequence 6, Application US/08978523		
CC	Sequence 6, Application US/08978523		
CC	Patent No. 5883229		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Guastella, John		
CC	TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2		
CC	TITLE OF INVENTION: Homologue		
CC	NUMBER OF SEQUENCES: 53		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.		
CC	STREET: 1100 New York Avenue, N.W., Suite 600		
CC	CITY: Washington		
CC	STATE: DC		
CC	COUNTRY: USA		
CC	ZIP: 20005		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: Patent In Release #1.0, Version #1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/978,523		
CC	FILING DATE: herewith		
CC	CLASSIFICATION: 424		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 08/798,897		
CC	FILING DATE: February 11, 1997		
CC	CLASSIFICATION: 424		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Esmond, Robert W.		
CC	REGISTRATION NUMBER: 32,893		
CC	REFERENCE/DOCKET NUMBER: 1483.0140002		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: 202-371-2600		
CC	TELEFAX: 202-371-2540		
CC	INFORMATION FOR SEQ ID NO: 6:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 192 amino acids		
CC	TYPE: amino acid		
CC	STRANDEDNESS: not relevant		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: protein		
SQ	SEQUENCE 192 AA; 20701 MW; 181510 CN;		
	Query Match 95.7%; Score 1326; DB 2; Length 192;		
	Best Local Similarity 94.3%; Pred. No. 2.75e-109;		
	Matches 181; Conservative 8; Mismatches 2; Indels 1; Gaps		
Db	1	ATPASADPTRALVEDFVGYKLQRKGVCYGAGPGEPAADPLHQAMRAAGD ² EFTFRRTTF	60
Qy	2	PTPASTDPTRALVADFVGYLRLQRKGVCYGAGPGEPAADPLHQAMRAAGD ² EFTFRRTTF	61

Db 1 MATPASADTRALVEDFYGYKLROKGYVCGAGPGEGPAADPLHOAMRAAGDEFEFRRT 60
QY 1 MPTPASTPDTRALVADFYGYRLROKGYVCGAGPGEGPAADPLHOAMRAAGDEFEFRRT 60
Db 61 FSDLAALHVTGPSAQORFTQVSDLEFQGGPNWGRVLAFFVFGAALCAESYNKEMEPLVG 120
QY 61 FSDLAALHVTGPSAQORFTQVSDLEFQGGPNWGRVLAFFVFGAALCAESYNKEMEPLVG 120
Db 121 QVQEWVAYLETRLDADTHSSGGWAEFTALYGDGALEEARLRREGNWA-SVTVVTGVAL 180
QY 121 QVQDWIVAYLETRLDADTHSSGGWAEFTALYGDGALEEARLRREGNWA-SVTVVTGVAL 179
Db 181 GALVTVGAFASK 193
QY 180 GALVTVGAFASK 192

RESULT 4
ID US-08-978-523-4 STANDARD; PRT; 193 AA.

XX xxxxxx

AC xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

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XX xxxxxx

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XX xxxxxx

Sequence 4, Application US/08978523

Sequence 4, Application US/08978523

Patent No. 5883229

GENERAL INFORMATION:

APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,523

FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140002

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 193 AA; 20832 MW; 183365 CN;

Query Match 96.5%; Score 1337; DB 2; Length 193;

Best Local Similarity 94.3%; Pred. No. 2.65e-110;

Matches 182; Conservative 8; Mismatches 2; Indels 1; Gaps 1;

Db 1 MATPASADTRALVEDFYGYKLROKGYVCGAGPGEGPAADPLHOAMRAAGDEFEFRRT 60
QY 1 MPTPASTPDTRALVADFYGYRLROKGYVCGAGPGEGPAADPLHOAMRAAGDEFEFRRT 60
Db 61 FSDLAALHVTGPSAQORFTQVSDLEFQGGPNWGRVLAFFVFGAALCAESYNKEMEPLVG 120
QY 61 FSDLAALHVTGPSAQORFTQVSDLEFQGGPNWGRVLAFFVFGAALCAESYNKEMEPLVG 120
Db 121 QVQEWVAYLETRLDADTHSSGGWAEFTALYGDGALEEARLRREGNWA-SVTVVTGVAL 180
QY 121 QVQDWIVAYLETRLDADTHSSGGWAEFTALYGDGALEEARLRREGNWA-SVTVVTGVAL 179
Db 181 GALVTVGAFASK 193
QY 180 GALVTVGAFASK 192

RESULT 5
ID US-08-978-523-5 STANDARD; PRT; 192 AA.

XX xxxxxx

AC xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

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Sequence 5, Application US/08978523

Sequence 5, Application US/08978523

Patent No. 5883229

GENERAL INFORMATION:

APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,523

FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140002

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 192 AA; 20689 MW; 183185 CN;

Query Match 96.1%; Score 1332; DB 2; Length 192;

Best Local Similarity 95.3%; Pred. No. 7.67e-110;

Matches 183; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

Query Match 96.9%; Score 1343; DB 1; Length 193;
Best Local Similarity 95.3%; Pred. No. 7.37e-111;
Matches 184; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

Db 1 MATPASTPTDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETFRRT 60
QY 1 MPTPASTPTDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETFRRT 60

Db 61 FSDLAQLHVTGPSAQORFTQVSDLELFOGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120
QY 61 FSDLAQLHVTGPSAQORFTQVSDLELFOGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120

Db 121 QVQDMWVYLETPLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTCAVAL 180
QY 121 QVQDMWVYLETPLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTCAVAL 180

Db 181 GALVTVGAFASK 193
QY 180 GALVTVGAFASK 192

RESULT 2
ID US-08-978-523-3 STANDARD; PRT; 193 AA.
XX
AC xxxxxx
DT
XX
DE
XX
Sequence 3, Application US/08978523
Sequence 3, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 193 AA; 20820 MW; 185063 CN;

Query Match 96.9%; Score 1343; DB 2; Length 193;
Best Local Similarity 95.3%; Pred. No. 7.37e-111;
Matches 184; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

Db 1 MATPASTPTDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETFRRT 60
QY 1 MPTPASTPTDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQAMRAAGDEFETFRRT 60

Db 61 FSDLAQLHVTGPSAQORFTQVSDLELFOGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120
QY 61 FSDLAQLHVTGPSAQORFTQVSDLELFOGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120

Db 121 QVQDMWVYLETPLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTCAVAL 180
QY 121 QVQDMWVYLETPLADWIHSSGGWAEFTALYDGALEEARLRREGNWSVRTVLTCAVAL 180

Db 181 GALVTVGAFASK 193
QY 180 GALVTVGAFASK 192

RESULT 3
ID US-08-798-897-4 STANDARD; PRT; 193 AA.
XX
AC xxxxxx
DT
XX
DE
XX
Sequence 4, Application US/08798897
Sequence 4, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 193 AA; 20832 MW; 183365 CN;

Query Match 96.5%; Score 1337; DB 1; Length 193;
Best Local Similarity 94.3%; Pred. No. 2.65e-110;
Matches 182; Conservative 8; Mismatches 2; Indels 1; Gaps 1;

